SEQUENCE LISTING

<110> Olmsted, Robert
       Keith, Paula
       Dryga, Sergey
       Caley, Ian
       Maughan, Maureen
       Johnston, Robert
       Davis, Nancy
       Swanstrom, Ronald

<120> ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE AS VACCINES

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<150> 09/902,537
<151> 2001-07-09

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<170> FastSEQ for Windows Version 4.0

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       synthetic construct

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<220>
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Thr Asp Asn Asp His Ala Asn Ala Arg Ala Phe Ser His Leu Ala Ser
         35                  40                  45

aaa ctg atc gaa acg gag gtg gac cca tcc gac acg atc ctt gac att       192
Lys Leu Ile Glu Thr Glu Val Asp Pro Ser Asp Thr Ile Leu Asp Ile
     50                  55                  60

gga agt gcg ccc gcc cgc aga atg tat tct aag cac aag tat cat tgt       240
Gly Ser Ala Pro Ala Arg Arg Met Tyr Ser Lys His Lys Tyr His Cys
 65                  70                  75                  80

atc tgt ccg atg aga tgt gcg gaa gat ccg gac aga ttg tat aag tat       288
Ile Cys Pro Met Arg Cys Ala Glu Asp Pro Asp Arg Leu Tyr Lys Tyr
                 85                  90                  95
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gca act aag ctg aag aaa aac tgt aag gaa ata act gat aag gaa ttg      336
Ala Thr Lys Leu Lys Lys Asn Cys Lys Glu Ile Thr Asp Lys Glu Leu
            100             105             110

gac aag aaa atg aag gag ctc gcc gcc gtc atg agc gac cct gac ctg      384
Asp Lys Lys Met Lys Glu Leu Ala Ala Val Met Ser Asp Pro Asp Leu
            115             120             125

gaa act gag act atg tgc ctc cac gac gac gag tcg tgt cgc tac gaa      432
Glu Thr Glu Thr Met Cys Leu His Asp Asp Glu Ser Cys Arg Tyr Glu
    130             135             140

ggg caa gtc gct gtt tac cag gat gta tac gcg gtt gac gga ccg aca      480
Gly Gln Val Ala Val Tyr Gln Asp Val Tyr Ala Val Asp Gly Pro Thr
145             150             155             160

agt ctc tat cac caa gcc aat aag gga gtt aga gtc gcc tac tgg ata      528
Ser Leu Tyr His Gln Ala Asn Lys Gly Val Arg Val Ala Tyr Trp Ile
            165             170             175

ggc ttt gac acc acc cct ttt atg ttt aag aac ttg gct gga gca tat      576
Gly Phe Asp Thr Thr Pro Phe Met Phe Lys Asn Leu Ala Gly Ala Tyr
            180             185             190

cca tca tac tct acc aac tgg gcc gac gaa acc gtg tta acg gct cgt      624
Pro Ser Tyr Ser Thr Asn Trp Ala Asp Glu Thr Val Leu Thr Ala Arg
            195             200             205

aac ata ggc cta tgc agc tct gac gtt atg gag cgg tca cgt aga ggg      672
Asn Ile Gly Leu Cys Ser Ser Asp Val Met Glu Arg Ser Arg Arg Gly
    210             215             220

atg tcc att ctt aga aag aag tat ttg aaa cca tcc aac aat gtt cta      720
Met Ser Ile Leu Arg Lys Lys Tyr Leu Lys Pro Ser Asn Asn Val Leu
225             230             235             240

ttc tct gtt ggc tcg acc atc tac cac gag aag agg gac tta ctg agg      768
Phe Ser Val Gly Ser Thr Ile Tyr His Glu Lys Arg Asp Leu Leu Arg
            245             250             255

agc tgg cac ctg ccg tct gta ttt cac tta cgt ggc aag caa aat tac      816
Ser Trp His Leu Pro Ser Val Phe His Leu Arg Gly Lys Gln Asn Tyr
            260             265             270

aca tgt cgg tgt gag act ata gtt agt tgc gac ggg tac gtc gtt aaa      864
Thr Cys Arg Cys Glu Thr Ile Val Ser Cys Asp Gly Tyr Val Val Lys
            275             280             285

aga ata gct atc agt cca ggc ctg tat ggg aag cct tca ggc tat gct      912
Arg Ile Ala Ile Ser Pro Gly Leu Tyr Gly Lys Pro Ser Gly Tyr Ala
    290             295             300

gct acg atg cac cgc gag gga ttc ttg tgc tgc aaa gtg aca gac aca      960
Ala Thr Met His Arg Glu Gly Phe Leu Cys Cys Lys Val Thr Asp Thr
305             310             315             320
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tta aac ggg gag agg gtc tct ttt ccc gtg tgc acg tat gtg cca gct    1008
Leu Asn Gly Glu Arg Val Ser Phe Pro Val Cys Thr Tyr Val Pro Ala
            325                 330                 335

aca ttg tgt gac caa atg act ggc ata ctg gca aca gat gtc agt gcg    1056
Thr Leu Cys Asp Gln Met Thr Gly Ile Leu Ala Thr Asp Val Ser Ala
            340                 345                 350

gac gac gcg caa aaa ctg ctg gtt ggg ctc aac cag cgt ata gtc gtc    1104
Asp Asp Ala Gln Lys Leu Leu Val Gly Leu Asn Gln Arg Ile Val Val
            355                 360                 365

aac ggt cgc acc cag aga aac acc aat acc atg aaa aat tac ctt ttg    1152
Asn Gly Arg Thr Gln Arg Asn Thr Asn Thr Met Lys Asn Tyr Leu Leu
    370                 375                 380

ccc gta gtg gcc cag gca ttt gct agg tgg gca aag gaa tat aag gaa    1200
Pro Val Val Ala Gln Ala Phe Ala Arg Trp Ala Lys Glu Tyr Lys Glu
385                 390                 395                 400

gat caa gaa gat gaa agg cca cta gga cta cga gat aga cag tta gtc    1248
Asp Gln Glu Asp Glu Arg Pro Leu Gly Leu Arg Asp Arg Gln Leu Val
            405                 410                 415

atg ggg tgt tgt tgg gct ttt aga agg cac aag ata aca tct att tat    1296
Met Gly Cys Cys Trp Ala Phe Arg Arg His Lys Ile Thr Ser Ile Tyr
            420                 425                 430

aag cgc ccg gat acc caa acc atc atc aaa gtg aac agc gat ttc cac    1344
Lys Arg Pro Asp Thr Gln Thr Ile Ile Lys Val Asn Ser Asp Phe His
            435                 440                 445

tca ttc gtg ctg ccc agg ata ggc agt aac aca ttg gag atc ggg ctg    1392
Ser Phe Val Leu Pro Arg Ile Gly Ser Asn Thr Leu Glu Ile Gly Leu
    450                 455                 460

aga aca aga atc agg aaa atg tta gag gag cac aag gag ccg tca cct    1440
Arg Thr Arg Ile Arg Lys Met Leu Glu Glu His Lys Glu Pro Ser Pro
465                 470                 475                 480

ctc att acc gcc gag gac gta caa gaa gct aag tgc gca gcc gat gag    1488
Leu Ile Thr Ala Glu Asp Val Gln Glu Ala Lys Cys Ala Ala Asp Glu
            485                 490                 495

gct aag gag gtg cgt gaa gcc gag gag ttg cgc gca gct cta cca cct    1536
Ala Lys Glu Val Arg Glu Ala Glu Glu Leu Arg Ala Ala Leu Pro Pro
            500                 505                 510

ttg gca gct gat gtt gag gag ccc act ctg gaa gcc gat gtc gac ttg    1584
Leu Ala Ala Asp Val Glu Glu Pro Thr Leu Glu Ala Asp Val Asp Leu
            515                 520                 525

atg tta caa gag gct ggg gcc ggc tca gtg gag aca cct cgt ggc ttg    1632
Met Leu Gln Glu Ala Gly Ala Gly Ser Val Glu Thr Pro Arg Gly Leu
    530                 535                 540
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ata aag gtt acc agc tac gct ggc gag gac aag atc ggc tct tac gct    1680
Ile Lys Val Thr Ser Tyr Ala Gly Glu Asp Lys Ile Gly Ser Tyr Ala
545             550             555             560


gtg ctt tct ccg cag gct gta ctc aag agt gaa aaa tta tct tgc atc    1728
Val Leu Ser Pro Gln Ala Val Leu Lys Ser Glu Lys Leu Ser Cys Ile
                565             570             575


cac cct ctc gct gaa caa gtc ata gtg ata aca cac tct ggc cga aaa    1776
His Pro Leu Ala Glu Gln Val Ile Val Ile Thr His Ser Gly Arg Lys
                580             585             590


ggg cgt tat gcc gtg gaa cca tac cat ggt aaa gta gtg gtg cca gag    1824
Gly Arg Tyr Ala Val Glu Pro Tyr His Gly Lys Val Val Val Pro Glu
            595             600             605


gga cat gca ata ccc gtc cag gac ttt caa gct ctg agt gaa agt gcc    1872
Gly His Ala Ile Pro Val Gln Asp Phe Gln Ala Leu Ser Glu Ser Ala
        610             615             620


acc att gtg tac aac gaa cgt gag ttc gta aac agg tac ctg cac cat    1920
Thr Ile Val Tyr Asn Glu Arg Glu Phe Val Asn Arg Tyr Leu His His
625             630             635             640


att gcc aca cat gga gga gcg ctg aac act gat gaa gaa tat tac aaa    1968
Ile Ala Thr His Gly Gly Ala Leu Asn Thr Asp Glu Glu Tyr Tyr Lys
                645             650             655


act gtc aag ccc agc gag cac gac ggc gaa tac ctg tac gac atc gac    2016
Thr Val Lys Pro Ser Glu His Asp Gly Glu Tyr Leu Tyr Asp Ile Asp
                660             665             670


agg aaa cag tgc gtc aag aaa gaa cta gtc act ggg cta ggg ctc aca    2064
Arg Lys Gln Cys Val Lys Lys Glu Leu Val Thr Gly Leu Gly Leu Thr
                675             680             685



ggc gag ctg gtg gat cct ccc ttc cat gaa ttc gcc tac gag agt ctg    2112
Gly Glu Leu Val Asp Pro Pro Phe His Glu Phe Ala Tyr Glu Ser Leu
        690             695             700


aga aca cga cca gcc gct cct tac caa gta cca acc ata ggg gtg tat    2160
Arg Thr Arg Pro Ala Ala Pro Tyr Gln Val Pro Thr Ile Gly Val Tyr
705             710             715             720


ggc gtg cca gga tca ggc aag tct ggc atc att aaa agc gca gtc acc    2208
Gly Val Pro Gly Ser Gly Lys Ser Gly Ile Ile Lys Ser Ala Val Thr
                725             730             735


aaa aaa gat cta gtg gtg agc gcc aag aaa gaa aac tgt gca gaa att    2256
Lys Lys Asp Leu Val Val Ser Ala Lys Lys Glu Asn Cys Ala Glu Ile
                740             745             750


ata agg gac gtc aag aaa atg aaa ggg ctg gac gtc aat gcc aga act    2304
Ile Arg Asp Val Lys Lys Met Lys Gly Leu Asp Val Asn Ala Arg Thr
                755             760             765
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gtg gac tca gtg ctc ttg aat gga tgc aaa cac ccc gta gag acc ctg        2352
Val Asp Ser Val Leu Leu Asn Gly Cys Lys His Pro Val Glu Thr Leu
    770              775              780

tat att gac gaa gct ttt gct tgt cat gca ggt act ctc aga gcg ctc        2400
Tyr Ile Asp Glu Ala Phe Ala Cys His Ala Gly Thr Leu Arg Ala Leu
785              790              795              800

ata gcc att ata aga cct aaa aag gca gtg ctc tgc ggg gat ccc aaa        2448
Ile Ala Ile Ile Arg Pro Lys Lys Ala Val Leu Cys Gly Asp Pro Lys
                 805              810              815

cag tgc ggt ttt ttt aac atg atg tgc ctg aaa gtg cat ttt aac cac        2496
Gln Cys Gly Phe Phe Asn Met Met Cys Leu Lys Val His Phe Asn His
             820              825              830

gag att tgc aca caa gtc ttc cac aaa agc atc tct cgc cgt tgc act        2544
Glu Ile Cys Thr Gln Val Phe His Lys Ser Ile Ser Arg Arg Cys Thr
             835              840              845

aaa tct gtg act tcg gtc gtc tca acc ttg ttt tac gac aaa aaa atg        2592
Lys Ser Val Thr Ser Val Val Ser Thr Leu Phe Tyr Asp Lys Lys Met
    850              855              860

aga acg acg aat ccg aaa gag act aag att gtg att gac act acc ggc        2640
Arg Thr Thr Asn Pro Lys Glu Thr Lys Ile Val Ile Asp Thr Thr Gly
865              870              875              880

agt acc aaa cct aag cag gac gat ctc att ctc act tgt ttc aga ggg        2688
Ser Thr Lys Pro Lys Gln Asp Asp Leu Ile Leu Thr Cys Phe Arg Gly
             885              890              895

tgg gtg aag cag ttg caa ata gat tac aaa ggc aac gaa ata atg acg        2736
Trp Val Lys Gln Leu Gln Ile Asp Tyr Lys Gly Asn Glu Ile Met Thr
             900              905              910

gca gct gcc tct caa ggg ctg acc cgt aaa ggt gtg tat gcc gtt cgg        2784
Ala Ala Ala Ser Gln Gly Leu Thr Arg Lys Gly Val Tyr Ala Val Arg
             915              920              925

tac aag gtg aat gaa aat cct ctg tac gca ccc acc tca gaa cat gtg        2832
Tyr Lys Val Asn Glu Asn Pro Leu Tyr Ala Pro Thr Ser Glu His Val
    930              935              940

aac gtc cta ctg acc cgc acg gag gac cgc atc gtg tgg aaa aca cta        2880
Asn Val Leu Leu Thr Arg Thr Glu Asp Arg Ile Val Trp Lys Thr Leu
945              950              955              960

gcc ggc gac cca tgg ata aaa aca ctg act gcc aag tac cct ggg aat        2928
Ala Gly Asp Pro Trp Ile Lys Thr Leu Thr Ala Lys Tyr Pro Gly Asn
             965              970              975

ttc act gcc acg ata gag gag tgg caa gca gag cat gat gcc atc atg        2976
Phe Thr Ala Thr Ile Glu Glu Trp Gln Ala Glu His Asp Ala Ile Met
             980              985              990
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agg cac atc ttg gag aga ccg gac cct acc gac gtc ttc cag aat aag      3024
Arg His Ile Leu Glu Arg Pro Asp Pro Thr Asp Val Phe Gln Asn Lys
        995                 1000                1005

gca aac gtg tgt tgg gcc aag gct tta gtg ccg gtg ctg aag acc gct      3072
Ala Asn Val Cys Trp Ala Lys Ala Leu Val Pro Val Leu Lys Thr Ala
        1010                1015                1020

ggc ata gac atg acc act gaa caa tgg aac act gtg gat tat ttt gaa      3120
Gly Ile Asp Met Thr Thr Glu Gln Trp Asn Thr Val Asp Tyr Phe Glu
1025                1030                1035                1040

acg gac aaa gct cac tca gca gag ata gta ttg aac caa cta tgc gtg      3168
Thr Asp Lys Ala His Ser Ala Glu Ile Val Leu Asn Gln Leu Cys Val
                1045                1050                1055

agg ttc ttt gga ctc gat ctg gac tcc ggt cta ttt tct gca ccc act      3216
Arg Phe Phe Gly Leu Asp Leu Asp Ser Gly Leu Phe Ser Ala Pro Thr
                1060                1065                1070

gtt ccg tta tcc att agg aat aat cac tgg gat aac tcc ccg tcg cct      3264
Val Pro Leu Ser Ile Arg Asn Asn His Trp Asp Asn Ser Pro Ser Pro
                1075                1080                1085

aac atg tac ggg ctg aat aaa gaa gtg gtc cgt cag ctc tct cgc agg      3312
Asn Met Tyr Gly Leu Asn Lys Glu Val Val Arg Gln Leu Ser Arg Arg
        1090                1095                1100


tac cca caa ctg cct cgg gca gtt gcc act gga aga gtc tat gac atg      3360
Tyr Pro Gln Leu Pro Arg Ala Val Ala Thr Gly Arg Val Tyr Asp Met
1105                1110                1115                1120

aac act ggt aca ctg cgc aat tat gat ccg cgc ata aac cta gta cct      3408
Asn Thr Gly Thr Leu Arg Asn Tyr Asp Pro Arg Ile Asn Leu Val Pro
                1125                1130                1135

gta aac aga aga ctg cct cat gct tta gtc ctc cac cat aat gaa cac      3456
Val Asn Arg Arg Leu Pro His Ala Leu Val Leu His His Asn Glu His
                1140                1145                1150

cca cag agt gac ttt tct tca ttc gtc agc aaa ttg aag ggc aga act      3504
Pro Gln Ser Asp Phe Ser Ser Phe Val Ser Lys Leu Lys Gly Arg Thr
                1155                1160                1165

gtc ctg gtg gtc ggg gaa aag ttg tcc gtc cca ggc aaa atg gtt gac      3552
Val Leu Val Val Gly Glu Lys Leu Ser Val Pro Gly Lys Met Val Asp
        1170                1175                1180

tgg ttg tca gac cgg cct gag gct acc ttc aga gct cgg ctg gat tta      3600
Trp Leu Ser Asp Arg Pro Glu Ala Thr Phe Arg Ala Arg Leu Asp Leu
1185                1190                1195                1200

ggc atc cca ggt gat gtg ccc aaa tat gac ata ata ttt gtt aat gtg      3648
Gly Ile Pro Gly Asp Val Pro Lys Tyr Asp Ile Ile Phe Val Asn Val
                1205                1210                1215
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agg acc cca tat aaa tac cat cac tat cag cag tgt gaa gac cat gcc      3696
Arg Thr Pro Tyr Lys Tyr His His Tyr Gln Gln Cys Glu Asp His Ala
        1220            1225                1230

att aag ctt agc atg ttg acc aag aaa gct tgt ctg cat ctg aat ccc      3744
Ile Lys Leu Ser Met Leu Thr Lys Lys Ala Cys Leu His Leu Asn Pro
        1235            1240                1245

ggc gga acc tgt gtc agc ata ggt tat ggt tac gct gac agg gcc agc      3792
Gly Gly Thr Cys Val Ser Ile Gly Tyr Gly Tyr Ala Asp Arg Ala Ser
        1250            1255                1260

gaa agc atc att ggt gct ata gcg cgg cag ttc aag ttt tcc cgg gta      3840
Glu Ser Ile Ile Gly Ala Ile Ala Arg Gln Phe Lys Phe Ser Arg Val
1265            1270                1275                1280

tgc aaa ccg aaa tcc tca ctt gaa gag acg gaa gtt ctg ttt gta ttc      3888
Cys Lys Pro Lys Ser Ser Leu Glu Glu Thr Glu Val Leu Phe Val Phe
                1285            1290                1295

att ggg tac gat cgc aag gcc cgt acg cac aat cct tac aag ctt tca      3936
Ile Gly Tyr Asp Arg Lys Ala Arg Thr His Asn Pro Tyr Lys Leu Ser
            1300            1305                1310


tca acc ttg acc aac att tat aca ggt tcc aga ctc cac gaa gcc gga      3984
Ser Thr Leu Thr Asn Ile Tyr Thr Gly Ser Arg Leu His Glu Ala Gly
            1315            1320                1325

tgt gca ccc tca tat cat gtg gtg cga ggg gat att gcc acg gcc acc      4032
Cys Ala Pro Ser Tyr His Val Val Arg Gly Asp Ile Ala Thr Ala Thr
        1330            1335                1340

gaa gga gtg att ata aat gct gct aac agc aaa gga caa cct ggc gga      4080
Glu Gly Val Ile Ile Asn Ala Ala Asn Ser Lys Gly Gln Pro Gly Gly
1345            1350                1355                1360

ggg gtg tgc gga gcg ctg tat aag aag ttc ccg gaa agc ttc gat tta      4128
Gly Val Cys Gly Ala Leu Tyr Lys Lys Phe Pro Glu Ser Phe Asp Leu
                1365            1370                1375

cag ccg atc gaa gta gga aaa gcg cga ctg gtc aaa ggt gca gct aaa      4176
Gln Pro Ile Glu Val Gly Lys Ala Arg Leu Val Lys Gly Ala Ala Lys
            1380            1385                1390

cat atc att cat gcc gta gga cca aac ttc aac aaa gtt tcg gag gtt      4224
His Ile Ile His Ala Val Gly Pro Asn Phe Asn Lys Val Ser Glu Val
            1395            1400                1405

gaa ggt gac aaa cag ttg gca gag gct tat gag tcc atc gct aag att      4272
Glu Gly Asp Lys Gln Leu Ala Glu Ala Tyr Glu Ser Ile Ala Lys Ile
        1410            1415                1420

gtc aac gat aac aat tac aag tca gta gcg att cca ctg ttg tcc acc      4320
Val Asn Asp Asn Asn Tyr Lys Ser Val Ala Ile Pro Leu Leu Ser Thr
1425            1430                1435                1440
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ggc atc ttt tcc ggg aac aaa gat cga cta acc caa tca ttg aac cat      4368
Gly Ile Phe Ser Gly Asn Lys Asp Arg Leu Thr Gln Ser Leu Asn His
            1445                1450                1455

ttg ctg aca gct tta gac acc act gat gca gat gta gcc ata tac tgc      4416
Leu Leu Thr Ala Leu Asp Thr Thr Asp Ala Asp Val Ala Ile Tyr Cys
            1460                1465                1470

agg gac aag aaa tgg gaa atg act ctc aag gaa gca gtg gct agg aga      4464
Arg Asp Lys Lys Trp Glu Met Thr Leu Lys Glu Ala Val Ala Arg Arg
            1475                1480                1485

gaa gca gtg gag gag ata tgc ata tcc gac gac tct tca gtg aca gaa      4512
Glu Ala Val Glu Glu Ile Cys Ile Ser Asp Asp Ser Ser Val Thr Glu
            1490                1495                1500

cct gat gca gag ctg gtg agg gtg cat ccg aag agt tct ttg gct gga      4560
Pro Asp Ala Glu Leu Val Arg Val His Pro Lys Ser Ser Leu Ala Gly
1505                1510                1515                1520


agg aag ggc tac agc aca agc gat ggc aaa act ttc tca tat ttg gaa      4608
Arg Lys Gly Tyr Ser Thr Ser Asp Gly Lys Thr Phe Ser Tyr Leu Glu
            1525                1530                1535

ggg acc aag ttt cac cag gcg gcc aag gat ata gca gaa att aat gcc      4656
Gly Thr Lys Phe His Gln Ala Ala Lys Asp Ile Ala Glu Ile Asn Ala
            1540                1545                1550

atg tgg ccc gtt gca acg gag gcc aat gag cag gta tgc atg tat atc      4704
Met Trp Pro Val Ala Thr Glu Ala Asn Glu Gln Val Cys Met Tyr Ile
            1555                1560                1565

ctc gga gaa agc atg agc agt att agg tcg aaa tgc ccc gtc gaa gag      4752
Leu Gly Glu Ser Met Ser Ser Ile Arg Ser Lys Cys Pro Val Glu Glu
            1570                1575                1580

tcg gaa gcc tcc aca cca cct agc acg ctg cct tgc ttg tgc atc cat      4800
Ser Glu Ala Ser Thr Pro Pro Ser Thr Leu Pro Cys Leu Cys Ile His
1585                1590                1595                1600

gcc atg act cca gaa aga gta cag cgc cta aaa gcc tca cgt cca gaa      4848
Ala Met Thr Pro Glu Arg Val Gln Arg Leu Lys Ala Ser Arg Pro Glu
            1605                1610                1615

caa att act gtg tgc tca tcc ttt cca ttg ccg aag tat aga atc act      4896
Gln Ile Thr Val Cys Ser Ser Phe Pro Leu Pro Lys Tyr Arg Ile Thr
            1620                1625                1630

ggt gtg cag aag atc caa tgc tcc cag cct ata ttg ttc tca ccg aaa      4944
Gly Val Gln Lys Ile Gln Cys Ser Gln Pro Ile Leu Phe Ser Pro Lys
            1635                1640                1645

gtg cct gcg tat att cat cca agg aag tat ctc gtg gaa aca cca ccg      4992
Val Pro Ala Tyr Ile His Pro Arg Lys Tyr Leu Val Glu Thr Pro Pro
            1650                1655                1660
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gta gac gag act ccg gag cca tcg gca gag aac caa tcc aca gag ggg    5040
Val Asp Glu Thr Pro Glu Pro Ser Ala Glu Asn Gln Ser Thr Glu Gly
1665                1670                1675                1680


aca cct gaa caa cca cca ctt ata acc gag gat gag acc agg act aga    5088
Thr Pro Glu Gln Pro Pro Leu Ile Thr Glu Asp Glu Thr Arg Thr Arg
                    1685                1690                1695


acg cct gag ccg atc atc atc gaa gag gaa gaa gag gat agc ata agt    5136
Thr Pro Glu Pro Ile Ile Ile Glu Glu Glu Glu Glu Asp Ser Ile Ser
                1700                1705                1710


ttg ctg tca gat ggc ccg acc cac cag gtg ctg caa gtc gag gca gac    5184
Leu Leu Ser Asp Gly Pro Thr His Gln Val Leu Gln Val Glu Ala Asp
            1715                1720                1725


att cac ggg ccg ccc tct gta tct agc tca tcc tgg tcc att cct cat    5232
Ile His Gly Pro Pro Ser Val Ser Ser Ser Trp Ser Ile Pro His
        1730                1735                1740


gca tcc gac ttt gat gtg gac agt tta tcc ata ctt gac acc ctg gag    5280
Ala Ser Asp Phe Asp Val Asp Ser Leu Ser Ile Leu Asp Thr Leu Glu
1745                1750                1755                1760


gga gct agc gtg acc agc ggg gca acg tca gcc gag act aac tct tac    5328
Gly Ala Ser Val Thr Ser Gly Ala Thr Ser Ala Glu Thr Asn Ser Tyr
                    1765                1770                1775


ttc gca aag agt atg gag ttt ctg gcg cga ccg gtg cct gcg cct cga    5376
Phe Ala Lys Ser Met Glu Phe Leu Ala Arg Pro Val Pro Ala Pro Arg
                1780                1785                1790


aca gta ttc agg aac cct cca cat ccc gct ccg cgc aca aga aca ccg    5424
Thr Val Phe Arg Asn Pro Pro His Pro Ala Pro Arg Thr Arg Thr Pro
                1795                1800                1805


tca ctt gca ccc agc agg gcc tgc tcg aga acc agc cta gtt tcc acc    5472
Ser Leu Ala Pro Ser Arg Ala Cys Ser Arg Thr Ser Leu Val Ser Thr
        1810                1815                1820

ccg cca ggc gtg aat agg gtg atc act aga gag gag ctc gag gcg ctt    5520
Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Leu Glu Ala Leu
1825                1830                1835                1840

acc ccg tca cgc act cct agc agg tcg gtc tcg aga acc agc ctg gtc    5568
Thr Pro Ser Arg Thr Pro Ser Arg Ser Val Ser Arg Thr Ser Leu Val
                1845                1850                1855


tcc aac ccg cca ggc gta aat agg gtg att aca aga gag gag ttt gag    5616
Ser Asn Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Phe Glu
                1860                1865                1870


gcg ttc gta gca caa caa caa tga cgg ttt gat gcg ggt gca tac atc    5664
Ala Phe Val Ala Gln Gln Gln  *  Arg Phe Asp Ala Gly Ala Tyr Ile
        1875                1880                1885
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ttt tcc tcc gac acc ggt caa ggg cat tta caa caa aaa tca gta agg      5712
Phe Ser Ser Asp Thr Gly Gln Gly His Leu Gln Gln Lys Ser Val Arg
        1890                1895                1900

caa acg gtg cta tcc gaa gtg gtg ttg gag agg acc gaa ttg gag att      5760
Gln Thr Val Leu Ser Glu Val Val Leu Glu Arg Thr Glu Leu Glu Ile
        1905                1910                1915

tcg tat gcc ccg cgc ctc gac caa gaa aaa gaa gaa tta cta cgc aag      5808
Ser Tyr Ala Pro Arg Leu Asp Gln Glu Lys Glu Glu Leu Leu Arg Lys
1920                1925                1930                1935

aaa tta cag tta aat ccc aca cct gct aac aga agc aga tac cag tcc      5856
Lys Leu Gln Leu Asn Pro Thr Pro Ala Asn Arg Ser Arg Tyr Gln Ser
                1940                1945                1950

agg aag gtg gag aac atg aaa gcc ata aca gct aga cgt att ctg caa      5904
Arg Lys Val Glu Asn Met Lys Ala Ile Thr Ala Arg Arg Ile Leu Gln
            1955                1960                1965

ggc cta ggg cat tat ttg aag gca gaa gga aaa gtg gag tgc tac cga      5952
Gly Leu Gly His Tyr Leu Lys Ala Glu Gly Lys Val Glu Cys Tyr Arg
            1970                1975                1980

acc ctg cat cct gtt cct ttg tat tca tct agt gtg aac cgt gcc ttt      6000
Thr Leu His Pro Val Pro Leu Tyr Ser Ser Ser Val Asn Arg Ala Phe
    1985                1990                1995

tca agc ccc aag gtc gca gtg gaa gcc tgt aac gcc atg ttg aaa gag      6048
Ser Ser Pro Lys Val Ala Val Glu Ala Cys Asn Ala Met Leu Lys Glu
2000                2005                2010                2015

aac ttt ccg act gtg gct tct tac tgt att att cca gag tac gat gcc      6096
Asn Phe Pro Thr Val Ala Ser Tyr Cys Ile Ile Pro Glu Tyr Asp Ala
                2020                2025                2030

tat ttg gac atg gtt gac gga gct tca tgc tgc tta gac act gcc agt      6144
Tyr Leu Asp Met Val Asp Gly Ala Ser Cys Cys Leu Asp Thr Ala Ser
            2035                2040                2045
ttt tgc cct gca aag ctg cgc agc ttt cca aag aaa cac tcc tat ttg      6192
Phe Cys Pro Ala Lys Leu Arg Ser Phe Pro Lys Lys His Ser Tyr Leu
            2050                2055                2060
gaa ccc aca ata cga tcg gca gtg cct tca gcg atc cag aac acg ctc      6240
Glu Pro Thr Ile Arg Ser Ala Val Pro Ser Ala Ile Gln Asn Thr Leu
    2065                2070                2075

cag aac gtc ctg gca gct gcc aca aaa aga aat tgc aat gtc acg caa      6288
Gln Asn Val Leu Ala Ala Ala Thr Lys Arg Asn Cys Asn Val Thr Gln
2080                2085                2090                2095

atg aga gaa ttg ccc gta ttg gat tcg gcg gcc ttt aat gtg gaa tgc      6336
Met Arg Glu Leu Pro Val Leu Asp Ser Ala Ala Phe Asn Val Glu Cys
                2100                2105                2110

ttc aag aaa tat gcg tgt aat aat gaa tat tgg gaa acg ttt aaa gaa      6384
Phe Lys Lys Tyr Ala Cys Asn Asn Glu Tyr Trp Glu Thr Phe Lys Glu
            2115                2120                2125
```

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aac ccc atc agg ctt act gaa gaa aac gtg gta aat tac att acc aaa      6432
Asn Pro Ile Arg Leu Thr Glu Glu Asn Val Val Asn Tyr Ile Thr Lys
        2130                2135                2140

tta aaa gga cca aaa gct gct gct ctt ttt gcg aag aca cat aat ttg      6480
Leu Lys Gly Pro Lys Ala Ala Ala Leu Phe Ala Lys Thr His Asn Leu
        2145                2150                2155

aat atg ttg cag gac ata cca atg gac agg ttt gta atg gac tta aag      6528
Asn Met Leu Gln Asp Ile Pro Met Asp Arg Phe Val Met Asp Leu Lys
2160                2165                2170                2175

aga gac gtg aaa gtg act cca gga aca aaa cat act gaa gaa cgg ccc      6576
Arg Asp Val Lys Val Thr Pro Gly Thr Lys His Thr Glu Glu Arg Pro
                2180                2185                2190

aag gta cag gtg atc cag gct gcc gat ccg cta gca aca gcg tat ctg      6624
Lys Val Gln Val Ile Gln Ala Ala Asp Pro Leu Ala Thr Ala Tyr Leu
                2195                2200                2205

tgc gga atc cac cga gag ctg gtt agg aga tta aat gcg gtc ctg ctt      6672
Cys Gly Ile His Arg Glu Leu Val Arg Arg Leu Asn Ala Val Leu Leu
        2210                2215                2220

ccg aac att cat aca ctg ttt gat atg tcg gct gaa gac ttt gac gct      6720
Pro Asn Ile His Thr Leu Phe Asp Met Ser Ala Glu Asp Phe Asp Ala
        2225                2230                2235

att ata gcc gag cac ttc cag cct ggg gat tgt gtt ctg gaa act gac      6768
Ile Ile Ala Glu His Phe Gln Pro Gly Asp Cys Val Leu Glu Thr Asp
2240                2245                2250                2255

atc gcg tcg ttt gat aaa agt gag gac gac gcc atg gct ctg acc gcg      6816
Ile Ala Ser Phe Asp Lys Ser Glu Asp Asp Ala Met Ala Leu Thr Ala
                2260                2265                2270

tta atg att ctg gaa gac tta ggt gtg gac gca gag ctg ttg acg ctg      6864
Leu Met Ile Leu Glu Asp Leu Gly Val Asp Ala Glu Leu Leu Thr Leu
                2275                2280                2285

att gag gcg gct ttc ggc gaa att tca tca ata cat ttg ccc act aaa      6912
Ile Glu Ala Ala Phe Gly Glu Ile Ser Ser Ile His Leu Pro Thr Lys
        2290                2295                2300

act aaa ttt aaa ttc gga gcc atg atg aaa tct gga atg ttc ctc aca      6960
Thr Lys Phe Lys Phe Gly Ala Met Met Lys Ser Gly Met Phe Leu Thr
        2305                2310                2315

ctg ttt gtg aac aca gtc att aac att gta atc gca agc aga gtg ttg      7008
Leu Phe Val Asn Thr Val Ile Asn Ile Val Ile Ala Ser Arg Val Leu
2320                2325                2330                2335

aga gaa cgg cta acc gga tca cca tgt gca gca ttc att gga gat gac      7056
Arg Glu Arg Leu Thr Gly Ser Pro Cys Ala Ala Phe Ile Gly Asp Asp
                2340                2345                2350

aat atc gtg aaa gga gtc aaa tcg gac aaa tta atg gca gac agg tgc      7104
Asn Ile Val Lys Gly Val Lys Ser Asp Lys Leu Met Ala Asp Arg Cys
                2355                2360                2365
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gcc acc tgg ttg aat atg gaa gtc aag att ata gat gct gtg gtg ggc      7152
Ala Thr Trp Leu Asn Met Glu Val Lys Ile Ile Asp Ala Val Val Gly
        2370              2375              2380

gag aaa gcg ccc tat ttc tgt gga ggg ttt att ttg tgt gac tcc gtg      7200
Glu Lys Ala Pro Tyr Phe Cys Gly Gly Phe Ile Leu Cys Asp Ser Val
        2385              2390              2395

acc ggc aca gcg tgc cgt gtg gca gac ccc cta aaa agg ctg ttt aag      7248
Thr Gly Thr Ala Cys Arg Val Ala Asp Pro Leu Lys Arg Leu Phe Lys
2400              2405              2410              2415

ctt ggc aaa cct ctg gca gca gac gat gaa cat gat gat gac agg aga      7296
Leu Gly Lys Pro Leu Ala Ala Asp Asp Glu His Asp Asp Asp Arg Arg
                2420              2425              2430

agg gca ttg cat gaa gag tca aca cgc tgg aac cga gtg ggt att ctt      7344
Arg Ala Leu His Glu Glu Ser Thr Arg Trp Asn Arg Val Gly Ile Leu
            2435              2440              2445

tca gag ctg tgc aag gca gta gaa tca agg tat gaa acc gta gga act      7392
Ser Glu Leu Cys Lys Ala Val Glu Ser Arg Tyr Glu Thr Val Gly Thr
        2450              2455              2460

tcc atc ata gtt atg gcc atg act act cta gct agc agt gtt aaa tca      7440
Ser Ile Ile Val Met Ala Met Thr Thr Leu Ala Ser Ser Val Lys Ser
        2465              2470              2475

ttc agc tac ctg aga ggg gcc cct ata act ctc tac ggc                  7479
Phe Ser Tyr Leu Arg Gly Ala Pro Ile Thr Leu Tyr Gly
2480              2485              2490
```

```
<210> 3
<211> 2492
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 3
Met Glu Lys Val His Val Asp Ile Glu Glu Asp Ser Pro Phe Leu Arg
 1               5                  10                  15
Ala Leu Gln Arg Ser Phe Pro Gln Phe Glu Val Glu Ala Lys Gln Val
            20                  25                  30
Thr Asp Asn Asp His Ala Asn Ala Arg Ala Phe Ser His Leu Ala Ser
        35                  40                  45
Lys Leu Ile Glu Thr Glu Val Asp Pro Ser Asp Thr Ile Leu Asp Ile
     50                  55                  60
Gly Ser Ala Pro Ala Arg Arg Met Tyr Ser Lys Lys Tyr His Cys
65                  70                  75                  80
Ile Cys Pro Met Arg Cys Ala Glu Asp Pro Asp Arg Leu Tyr Lys Tyr
                85                  90                  95
Ala Thr Lys Leu Lys Lys Asn Cys Lys Glu Ile Thr Asp Lys Glu Leu
            100                 105                 110
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Asp Lys Lys Met Lys Glu Leu Ala Ala Val Met Ser Asp Pro Asp Leu
        115             120             125
Glu Thr Glu Thr Met Cys Leu His Asp Asp Glu Ser Cys Arg Tyr Glu
    130                 135             140

Gly Gln Val Ala Val Tyr Gln Asp Val Tyr Ala Val Asp Gly Pro Thr
145                 150             155                 160
Ser Leu Tyr His Gln Ala Asn Lys Gly Val Arg Val Ala Tyr Trp Ile
            165             170             175
Gly Phe Asp Thr Thr Pro Phe Met Phe Lys Asn Leu Ala Gly Ala Tyr
            180             185             190
Pro Ser Tyr Ser Thr Asn Trp Ala Asp Glu Thr Val Leu Thr Ala Arg
        195             200             205
Asn Ile Gly Leu Cys Ser Ser Asp Val Met Glu Arg Ser Arg Arg Gly
    210             215             220
Met Ser Ile Leu Arg Lys Lys Tyr Leu Lys Pro Ser Asn Asn Val Leu
225             230             235             240
Phe Ser Val Gly Ser Thr Ile Tyr His Glu Lys Arg Asp Leu Leu Arg
            245             250             255
Ser Trp His Leu Pro Ser Val Phe His Leu Arg Gly Lys Gln Asn Tyr
            260             265             270
Thr Cys Arg Cys Glu Thr Ile Val Ser Cys Asp Gly Tyr Val Val Lys
            275             280             285
Arg Ile Ala Ile Ser Pro Gly Leu Tyr Gly Lys Pro Ser Gly Tyr Ala
    290             295             300
Ala Thr Met His Arg Glu Gly Phe Leu Cys Cys Lys Val Thr Asp Thr
305             310             315             320
Leu Asn Gly Glu Arg Val Ser Phe Pro Val Cys Thr Tyr Val Pro Ala
            325             330             335
Thr Leu Cys Asp Gln Met Thr Gly Ile Leu Ala Thr Asp Val Ser Ala
            340             345             350
Asp Asp Ala Gln Lys Leu Leu Val Gly Leu Asn Gln Arg Ile Val Val
            355             360             365
Asn Gly Arg Thr Gln Arg Asn Thr Asn Thr Met Lys Asn Tyr Leu Leu
    370             375             380
Pro Val Val Ala Gln Ala Phe Ala Arg Trp Ala Lys Glu Tyr Lys Glu
385             390             395             400
Asp Gln Glu Asp Glu Arg Pro Leu Gly Leu Arg Asp Arg Gln Leu Val
            405             410             415
Met Gly Cys Cys Trp Ala Phe Arg Arg His Lys Ile Thr Ser Ile Tyr
            420             425             430
Lys Arg Pro Asp Thr Gln Thr Ile Ile Lys Val Asn Ser Asp Phe His
        435             440             445
Ser Phe Val Leu Pro Arg Ile Gly Ser Asn Thr Leu Glu Ile Gly Leu
    450             455             460
Arg Thr Arg Ile Arg Lys Met Leu Glu Glu His Lys Glu Pro Ser Pro
465             470             475             480
Leu Ile Thr Ala Glu Asp Val Gln Glu Ala Lys Cys Ala Ala Asp Glu
            485             490             495
Ala Lys Glu Val Arg Glu Ala Glu Glu Leu Arg Ala Ala Leu Pro Pro
            500             505             510
Leu Ala Ala Asp Val Glu Glu Pro Thr Leu Glu Ala Asp Val Asp Leu
            515             520             525
Met Leu Gln Glu Ala Gly Ala Gly Ser Val Glu Thr Pro Arg Gly Leu
            530             535             540
Ile Lys Val Thr Ser Tyr Ala Gly Glu Asp Lys Ile Gly Ser Tyr Ala
545                 550             555                 560
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Val Leu Ser Pro Gln Ala Val Leu Lys Ser Glu Lys Leu Ser Cys Ile
            565                 570                 575
His Pro Leu Ala Glu Gln Val Ile Val Ile Thr His Ser Gly Arg Lys
            580                 585                 590
Gly Arg Tyr Ala Val Glu Pro Tyr His Gly Lys Val Val Val Pro Glu
            595                 600                 605
Gly His Ala Ile Pro Val Gln Asp Phe Gln Ala Leu Ser Glu Ser Ala
    610                 615                 620
Thr Ile Val Tyr Asn Glu Arg Glu Phe Val Asn Arg Tyr Leu His His
625                 630                 635                 640
Ile Ala Thr His Gly Gly Ala Leu Asn Thr Asp Glu Glu Tyr Tyr Lys
            645                 650                 655
Thr Val Lys Pro Ser Glu His Asp Gly Glu Tyr Leu Tyr Asp Ile Asp
            660                 665                 670
Arg Lys Gln Cys Val Lys Lys Glu Leu Val Thr Gly Leu Gly Leu Thr
            675                 680                 685
Gly Glu Leu Val Asp Pro Pro Phe His Glu Phe Ala Tyr Glu Ser Leu
    690                 695                 700
Arg Thr Arg Pro Ala Ala Pro Tyr Gln Val Pro Thr Ile Gly Val Tyr
705                 710                 715                 720
Gly Val Pro Gly Ser Gly Lys Ser Gly Ile Ile Lys Ser Ala Val Thr
            725                 730                 735
Lys Lys Asp Leu Val Val Ser Ala Lys Lys Glu Asn Cys Ala Glu Ile
            740                 745                 750
Ile Arg Asp Val Lys Lys Met Lys Gly Leu Asp Val Asn Ala Arg Thr
            755                 760                 765
Val Asp Ser Val Leu Leu Asn Gly Cys Lys His Pro Val Glu Thr Leu
    770                 775                 780
Tyr Ile Asp Glu Ala Phe Ala Cys His Ala Gly Thr Leu Arg Ala Leu
785                 790                 795                 800
Ile Ala Ile Ile Arg Pro Lys Lys Ala Val Leu Cys Gly Asp Pro Lys
            805                 810                 815
Gln Cys Gly Phe Phe Asn Met Met Cys Leu Lys Val His Phe Asn His
            820                 825                 830

Glu Ile Cys Thr Gln Val Phe His Lys Ser Ile Ser Arg Arg Cys Thr
            835                 840                 845
Lys Ser Val Thr Ser Val Val Ser Thr Leu Phe Tyr Asp Lys Lys Met
850                 855                 860
Arg Thr Thr Asn Pro Lys Glu Thr Lys Ile Val Ile Asp Thr Thr Gly
865                 870                 875                 880
Ser Thr Lys Pro Lys Gln Asp Asp Leu Ile Leu Thr Cys Phe Arg Gly
            885                 890                 895
Trp Val Lys Gln Leu Gln Ile Asp Tyr Lys Gly Asn Glu Ile Met Thr
            900                 905                 910
Ala Ala Ala Ser Gln Gly Leu Thr Arg Lys Gly Val Tyr Ala Val Arg
            915                 920                 925
Tyr Lys Val Asn Glu Asn Pro Leu Tyr Ala Pro Thr Ser Glu His Val
    930                 935                 940
Asn Val Leu Leu Thr Arg Thr Glu Asp Arg Ile Val Trp Lys Thr Leu
945                 950                 955                 960
Ala Gly Asp Pro Trp Ile Lys Thr Leu Thr Ala Lys Tyr Pro Gly Asn
            965                 970                 975
Phe Thr Ala Thr Ile Glu Glu Trp Gln Ala Glu His Asp Ala Ile Met
            980                 985                 990
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Arg His Ile Leu Glu Arg Pro Asp Pro Thr Asp Val Phe Gln Asn Lys
        995                 1000                1005
Ala Asn Val Cys Trp Ala Lys Ala Leu Val Pro Val Leu Lys Thr Ala
    1010                1015                1020
Gly Ile Asp Met Thr Thr Glu Gln Trp Asn Thr Val Asp Tyr Phe Glu
1025                1030                1035                1040
Thr Asp Lys Ala His Ser Ala Glu Ile Val Leu Asn Gln Leu Cys Val
            1045                1050                1055
Arg Phe Phe Gly Leu Asp Leu Asp Ser Gly Leu Phe Ser Ala Pro Thr
            1060                1065                1070
Val Pro Leu Ser Ile Arg Asn Asn His Trp Asp Asn Ser Pro Ser Pro
        1075                1080                1085
Asn Met Tyr Gly Leu Asn Lys Glu Val Val Arg Gln Leu Ser Arg Arg
    1090                1095                1100
Tyr Pro Gln Leu Pro Arg Ala Val Ala Thr Gly Arg Val Tyr Asp Met
1105                1110                1115                1120
Asn Thr Gly Thr Leu Arg Asn Tyr Asp Pro Arg Ile Asn Leu Val Pro
            1125                1130                1135
Val Asn Arg Arg Leu Pro His Ala Leu Val Leu His His Asn Glu His
            1140                1145                1150
Pro Gln Ser Asp Phe Ser Ser Phe Val Ser Lys Leu Lys Gly Arg Thr
        1155                1160                1165
Val Leu Val Val Gly Glu Lys Leu Ser Val Pro Gly Lys Met Val Asp
    1170                1175                1180
Trp Leu Ser Asp Arg Pro Glu Ala Thr Phe Arg Ala Arg Leu Asp Leu
1185                1190                1195                1200
Gly Ile Pro Gly Asp Val Pro Lys Tyr Asp Ile Ile Phe Val Asn Val
            1205                1210                1215
Arg Thr Pro Tyr Lys Tyr His His Tyr Gln Gln Cys Glu Asp His Ala
            1220                1225                1230
Ile Lys Leu Ser Met Leu Thr Lys Lys Ala Cys Leu His Leu Asn Pro
        1235                1240                1245
Gly Gly Thr Cys Val Ser Ile Gly Tyr Gly Tyr Ala Asp Arg Ala Ser
    1250                1255                1260

Glu Ser Ile Ile Gly Ala Ile Ala Arg Gln Phe Lys Phe Ser Arg Val
1265                1270                1275                1280
Cys Lys Pro Lys Ser Ser Leu Glu Glu Thr Glu Val Leu Phe Val Phe
            1285                1290                1295
Ile Gly Tyr Asp Arg Lys Ala Arg Thr His Asn Pro Tyr Lys Leu Ser
        1300                1305                1310
Ser Thr Leu Thr Asn Ile Tyr Thr Gly Ser Arg Leu His Glu Ala Gly
    1315                1320                1325
Cys Ala Pro Ser Tyr His Val Val Arg Gly Asp Ile Ala Thr Ala Thr
    1330                1335                1340
Glu Gly Val Ile Ile Asn Ala Ala Asn Ser Lys Gly Gln Pro Gly Gly
1345                1350                1355                1360
Gly Val Cys Gly Ala Leu Tyr Lys Lys Phe Pro Glu Ser Phe Asp Leu
            1365                1370                1375
Gln Pro Ile Glu Val Gly Lys Ala Arg Leu Val Lys Gly Ala Ala Lys
        1380                1385                1390
His Ile Ile His Ala Val Gly Pro Asn Phe Asn Lys Val Ser Glu Val
        1395                1400                1405

Glu Gly Asp Lys Gln Leu Ala Glu Ala Tyr Glu Ser Ile Ala Lys Ile
    1410                1415                1420
```

Val Asn Asp Asn Asn Tyr Lys Ser Val Ala Ile Pro Leu Leu Ser Thr
1425   1430   1435   1440
Gly Ile Phe Ser Gly Asn Lys Asp Arg Leu Thr Gln Ser Leu Asn His
          1445   1450   1455
Leu Leu Thr Ala Leu Asp Thr Thr Asp Ala Asp Val Ala Ile Tyr Cys
          1460   1465   1470
Arg Asp Lys Lys Trp Glu Met Thr Leu Lys Glu Ala Val Ala Arg Arg
          1475   1480   1485
Glu Ala Val Glu Glu Ile Cys Ile Ser Asp Asp Ser Ser Val Thr Glu
      1490   1495   1500
Pro Asp Ala Glu Leu Val Arg Val His Pro Lys Ser Ser Leu Ala Gly
1505   1510   1515   1520
Arg Lys Gly Tyr Ser Thr Ser Asp Gly Lys Thr Phe Ser Tyr Leu Glu
              1525   1530   1535
Gly Thr Lys Phe His Gln Ala Ala Lys Asp Ile Ala Glu Ile Asn Ala
          1540   1545   1550
Met Trp Pro Val Ala Thr Glu Ala Asn Glu Gln Val Cys Met Tyr Ile
          1555   1560   1565
Leu Gly Glu Ser Met Ser Ser Ile Arg Ser Lys Cys Pro Val Glu Glu
      1570   1575   1580
Ser Glu Ala Ser Thr Pro Pro Ser Thr Leu Pro Cys Leu Cys Ile His
1585   1590   1595   1600
Ala Met Thr Pro Glu Arg Val Gln Arg Leu Lys Ala Ser Arg Pro Glu
              1605   1610   1615
Gln Ile Thr Val Cys Ser Ser Phe Pro Leu Pro Lys Tyr Arg Ile Thr
          1620   1625   1630
Gly Val Gln Lys Ile Gln Cys Ser Gln Pro Ile Leu Phe Ser Pro Lys
          1635   1640   1645
Val Pro Ala Tyr Ile His Pro Arg Lys Tyr Leu Val Glu Thr Pro Pro
      1650   1655   1660
Val Asp Glu Thr Pro Glu Pro Ser Ala Glu Asn Gln Ser Thr Glu Gly
1665   1670   1675   1680
Thr Pro Glu Gln Pro Pro Leu Ile Thr Glu Asp Glu Thr Arg Thr Arg
              1685   1690   1695

Thr Pro Glu Pro Ile Ile Ile Glu Glu Glu Glu Asp Ser Ile Ser
          1700   1705   1710
Leu Leu Ser Asp Gly Pro Thr His Gln Val Leu Gln Val Glu Ala Asp
          1715   1720   1725
Ile His Gly Pro Pro Ser Val Ser Ser Ser Trp Ser Ile Pro His
      1730   1735   1740
Ala Ser Asp Phe Asp Val Asp Ser Leu Ser Ile Leu Asp Thr Leu Glu
1745   1750   1755   1760
Gly Ala Ser Val Thr Ser Gly Ala Thr Ser Ala Glu Thr Asn Ser Tyr
          1765   1770   1775
Phe Ala Lys Ser Met Glu Phe Leu Ala Arg Pro Val Pro Ala Pro Arg
          1780   1785   1790
Thr Val Phe Arg Asn Pro Pro His Pro Ala Pro Arg Thr Arg Thr Pro
          1795   1800   1805
Ser Leu Ala Pro Ser Arg Ala Cys Ser Arg Thr Ser Leu Val Ser Thr
      1810   1815   1820

Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Leu Glu Ala Leu
1825   1830   1835   1840
Thr Pro Ser Arg Thr Pro Ser Arg Ser Val Ser Arg Thr Ser Leu Val
              1845   1850   1855

Ser Asn Pro Pro Gly Val Asn Arg Val Ile Thr Arg Glu Glu Phe Glu
      1860   1865   1870

Ala Phe Val Ala Gln Gln Gln Arg Phe Asp Ala Gly Ala Tyr Ile Phe
      1875   1880   1885

Ser Ser Asp Thr Gly Gln Gly His Leu Gln Gln Lys Ser Val Arg Gln
1890   1895   1900

Thr Val Leu Ser Glu Val Val Leu Glu Arg Thr Glu Leu Glu Ile Ser
1905   1910   1915   1920

Tyr Ala Pro Arg Leu Asp Gln Glu Lys Glu Glu Leu Leu Arg Lys Lys
      1925   1930   1935

Leu Gln Leu Asn Pro Thr Pro Ala Asn Arg Ser Arg Tyr Gln Ser Arg
      1940   1945   1950

Lys Val Glu Asn Met Lys Ala Ile Thr Ala Arg Arg Ile Leu Gln Gly
      1955   1960   1965

Leu Gly His Tyr Leu Lys Ala Glu Gly Lys Val Glu Cys Tyr Arg Thr
      1970   1975   1980

Leu His Pro Val Pro Leu Tyr Ser Ser Ser Val Asn Arg Ala Phe Ser
1985   1990   1995   2000

Ser Pro Lys Val Ala Val Glu Ala Cys Asn Ala Met Leu Lys Glu Asn
      2005   2010   2015

Phe Pro Thr Val Ala Ser Tyr Cys Ile Ile Pro Glu Tyr Asp Ala Tyr
      2020   2025   2030

Leu Asp Met Val Asp Gly Ala Ser Cys Cys Leu Asp Thr Ala Ser Phe
      2035   2040   2045

Cys Pro Ala Lys Leu Arg Ser Phe Pro Lys Lys His Ser Tyr Leu Glu
      2050   2055   2060

Pro Thr Ile Arg Ser Ala Val Pro Ser Ala Ile Gln Asn Thr Leu Gln
2065   2070   2075   2080

Asn Val Leu Ala Ala Ala Thr Lys Arg Asn Cys Asn Val Thr Gln Met
      2085   2090   2095

Arg Glu Leu Pro Val Leu Asp Ser Ala Ala Phe Asn Val Glu Cys Phe
      2100   2105   2110

Lys Lys Tyr Ala Cys Asn Asn Glu Tyr Trp Glu Thr Phe Lys Glu Asn
      2115   2120   2125

Pro Ile Arg Leu Thr Glu Glu Asn Val Val Asn Tyr Ile Thr Lys Leu
      2130   2135   2140

Lys Gly Pro Lys Ala Ala Ala Leu Phe Ala Lys Thr His Asn Leu Asn
2145   2150   2155   2160

Met Leu Gln Asp Ile Pro Met Asp Arg Phe Val Met Asp Leu Lys Arg
      2165   2170   2175

Asp Val Lys Val Thr Pro Gly Thr Lys His Thr Glu Glu Arg Pro Lys
      2180   2185   2190

Val Gln Val Ile Gln Ala Ala Asp Pro Leu Ala Thr Ala Tyr Leu Cys
      2195   2200   2205

Gly Ile His Arg Glu Leu Val Arg Arg Leu Asn Ala Val Leu Leu Pro
      2210   2215   2220

Asn Ile His Thr Leu Phe Asp Met Ser Ala Glu Asp Phe Asp Ala Ile
2225   2230   2235   2240

Ile Ala Glu His Phe Gln Pro Gly Asp Cys Val Leu Glu Thr Asp Ile
      2245   2250   2255

Ala Ser Phe Asp Lys Ser Glu Asp Asp Ala Met Ala Leu Thr Ala Leu
      2260   2265   2270

Met Ile Leu Glu Asp Leu Gly Val Asp Ala Glu Leu Leu Thr Leu Ile
      2275   2280   2285

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Glu Ala Ala Phe Gly Glu Ile Ser Ser Ile His Leu Pro Thr Lys Thr
    2290              2295              2300
Lys Phe Lys Phe Gly Ala Met Met Lys Ser Gly Met Phe Leu Thr Leu
2305              2310              2315              2320
Phe Val Asn Thr Val Ile Asn Ile Val Ile Ala Ser Arg Val Leu Arg
             2325              2330              2335
Glu Arg Leu Thr Gly Ser Pro Cys Ala Ala Phe Ile Gly Asp Asp Asn
         2340              2345              2350
Ile Val Lys Gly Val Lys Ser Asp Lys Leu Met Ala Asp Arg Cys Ala
         2355              2360              2365
Thr Trp Leu Asn Met Glu Val Lys Ile Ile Asp Ala Val Val Gly Glu
    2370              2375              2380
Lys Ala Pro Tyr Phe Cys Gly Gly Phe Ile Leu Cys Asp Ser Val Thr
2385              2390              2395              2400
Gly Thr Ala Cys Arg Val Ala Asp Pro Leu Lys Arg Leu Phe Lys Leu
             2405              2410              2415
Gly Lys Pro Leu Ala Ala Asp Asp Glu His Asp Asp Asp Arg Arg Arg
         2420              2425              2430
Ala Leu His Glu Glu Ser Thr Arg Trp Asn Arg Val Gly Ile Leu Ser
         2435              2440              2445
Glu Leu Cys Lys Ala Val Glu Ser Arg Tyr Glu Thr Val Gly Thr Ser
    2450              2455              2460
Ile Ile Val Met Ala Met Thr Thr Leu Ala Ser Ser Val Lys Ser Phe
2465              2470              2475              2480
Ser Tyr Leu Arg Gly Ala Pro Ile Thr Leu Tyr Gly
         2485              2490


<210> 4
<211> 1476
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<221> CDS
<222> (1)...(1476)

<400> 4
atg gct gcg aga gcg tca ata tta aga ggg gaa aaa tta gat aaa tgg      48
Met Ala Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp
 1               5                  10                  15

gaa aag att agg tta agg cca ggg gga aag aaa cat tat atg tta aaa      96
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys
                20                  25                  30

cac ata gta tgg gcg agc agg gag ctg gaa aga ttt gca ctt aac cct    144
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Leu Asn Pro
             35                  40                  45

ggc ctt tta gaa aca tca gaa gga tgt aaa caa ata atg aaa cag cta    192
Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Met Lys Gln Leu
     50                  55                  60
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caa cca gct ctc cag aca gga aca gag gaa ctt aaa tca tta tac aac      240
Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Lys Ser Leu Tyr Asn
65                      70                  75                  80

aca gta gca act ctc tat tgt gta cat gaa aag ata gaa gta cga gac      288
Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp
                    85                  90                  95

acc aag gaa gcc tta gat aag ata gag gaa gaa caa aac aaa tgt cag      336
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln
                100                 105                 110

caa aaa acg cag cag gca aaa gcg gct gac ggg aaa gtc agt caa aat      384
Gln Lys Thr Gln Gln Ala Lys Ala Ala Asp Gly Lys Val Ser Gln Asn
            115                 120                 125

tat cct ata gtg cag aat ctc caa ggg caa atg gta cat caa gcc ata      432
Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile
        130                 135                 140

tca cct aga acc ttg aat gca tgg gta aaa gta ata gaa gaa aag gct      480
Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala
145                 150                 155                 160

ttt agc cca gag gta ata ccc atg ttt aca gca tta tca gaa gga gcc      528
Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala
                    165                 170                 175

acc cca caa gat tta aac acc atg tta aat aca gtg ggg gga cac caa      576
Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
                180                 185                 190

gca gcc atg caa atg tta aaa gat act att aat gaa gag gct gca gaa      624
Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu
            195                 200                 205

tgg gat aga tta cat cca gtc cat gcg ggg cct att gca cca ggc cag      672
Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
        210                 215                 220

atg aga gaa cca agg gga agt gac ata gca gga act act agt acc ctt      720
Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
225                 230                 235                 240


cag gaa caa ata gca tgg atg aca agt aac cca cct att cca gtg gga      768
Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val Gly
                    245                 250                 255

gac atc tat aaa aga tgg ata att ctg ggg tta aat aaa ata gtg aga      816
Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
                260                 265                 270

atg tat agc ccg gtc agc att ttg gac ata aga caa ggg cca aag gaa      864
Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
            275                 280                 285
```

```
ccc ttt cga gac tat gta gat cgg ttc ttt aaa act tta aga gct gaa        912
Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu
    290             295             300

caa gct aca caa gaa gta aaa aat tgg atg aca gac acc ttg tta gtc        960
Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu Val
305             310             315        .        320

caa aat gcg aac cca gat tgt aag acc att ttg aga gca tta gga cca      1008
Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro
            325             330             335

ggg gct aca tta gaa gaa atg atg aca gca tgt caa ggg gtg gga gga      1056
Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
        340             345             350

cct ggc cac aaa gca aga gta ttg gct gag gca atg agt caa aca aac      1104
Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Thr Asn
        355             360             365

agt gga aac ata atg atg cag aga agc aat ttt aaa ggc cct aga aga      1152
Ser Gly Asn Ile Met Met Gln Arg Ser Asn Phe Lys Gly Pro Arg Arg
    370             375             380

att gtt aaa tgt ttt aac tgt ggc aag gaa ggg cac ata gcc aga aat      1200
Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn
385             390             395             400

tgc aga gcc cct agg aaa aaa ggc tgt tgg aaa tgt gga aaa gaa gga      1248
Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
            405             410             415

cac caa atg aaa gac tgc act gag agg cag gct aat ttt tta ggg aaa      1296
His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
        420             425             430

att tgg cct tcc cac aag ggg agg cca ggg aat ttc ctt cag aac aga      1344
Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg
        435             440             445

cca gag cca aca gcc cca cca gca gag agc ttc agg ttc gaa gag aca      1392
Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr
    450             455             460

acc ccc gct ccg aaa cag gag ccg ata gaa agg gaa ccc tta act tcc      1440
Thr Pro Ala Pro Lys Gln Glu Pro Ile Glu Arg Glu Pro Leu Thr Ser
465             470             475             480

ctc aaa tca ctc ttt ggc agc gac ccc ttg tct caa                      1476
Leu Lys Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln
        485             490
```

```
<210> 5
<211> 492
<212> PRT
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 5
Met Ala Ala Arg Ala Ser Ile Leu Arg Gly Glu Lys Leu Asp Lys Trp
 1   5   10   15
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys His Tyr Met Leu Lys
                20   25   30
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Leu Asn Pro
            35   40   45
Gly Leu Leu Glu Thr Ser Glu Gly Cys Lys Gln Ile Met Lys Gln Leu
        50   55   60
Gln Pro Ala Leu Gln Thr Gly Thr Glu Glu Leu Lys Ser Leu Tyr Asn
65   70   75   80
Thr Val Ala Thr Leu Tyr Cys Val His Glu Lys Ile Glu Val Arg Asp
                85   90   95
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Cys Gln
                100   105   110
Gln Lys Thr Gln Gln Ala Lys Ala Ala Asp Gly Lys Val Ser Gln Asn
            115   120   125
Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met Val His Gln Ala Ile
    130   135   140
Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Ile Glu Glu Lys Ala
145   150   155   160
Phe Ser Pro Glu Val Ile Pro Met Phe Thr Ala Leu Ser Glu Gly Ala
                165   170   175
Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly His Gln
                180   185   190
Ala Ala Met Gln Met Leu Lys Asp Thr Ile Asn Glu Glu Ala Ala Glu
        195   200   205

Trp Asp Arg Leu His Pro Val His Ala Gly Pro Ile Ala Pro Gly Gln
    210   215   220
Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser Thr Leu
225   230   235   240
Gln Glu Gln Ile Ala Trp Met Thr Ser Asn Pro Pro Ile Pro Val Gly
                245   250   255
Asp Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg
                260   265   270
Met Tyr Ser Pro Val Ser Ile Leu Asp Ile Arg Gln Gly Pro Lys Glu
                275   280   285
Pro Phe Arg Asp Tyr Val Asp Arg Phe Phe Lys Thr Leu Arg Ala Glu
    290   295   300
Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr Asp Thr Leu Leu Val
305   310   315   320
Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Arg Ala Leu Gly Pro
                325   330   335
Gly Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly Val Gly Gly
            340   345   350
Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln Thr Asn
    355   360   365
Ser Gly Asn Ile Met Met Gln Arg Ser Asn Phe Lys Gly Pro Arg Arg
    370   375   380
Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Ile Ala Arg Asn
385   390   395   400

```
Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys Gly Lys Glu Gly
            405                 410                 415
His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn Phe Leu Gly Lys
            420                 425                 430
Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu Gln Asn Arg
            435                 440                 445
Pro Glu Pro Thr Ala Pro Pro Ala Glu Ser Phe Arg Phe Glu Glu Thr
        450                 455                 460
Thr Pro Ala Pro Lys Gln Glu Pro Ile Glu Arg Glu Pro Leu Thr Ser
465                 470                 475                 480
Leu Lys Ser Leu Phe Gly Ser Asp Pro Leu Ser Gln
                485                 490
```

<210> 6
<211> 813
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<221> CDS
<222> (1)...(813)

<400> 6
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atg agc cat att caa cgg gaa acg tct tgc tcg agg ccg cga tta aat    48
Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn
1               5                   10                  15


tcc aac atg gat gct gat tta tat ggg tat aaa tgg gct cgc gat aat    96
Ser Asn Met Asp Ala Asp Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn
                20                  25                  30


gtc ggg caa tca ggt gcg aca atc tat cga ttg tat ggg aag ccc gat   144
Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp
            35                  40                  45


gcg cca gag ttg ttt ctg aaa cat ggc aaa ggt agc gtt gcc aat gat   192
Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp
        50                  55                  60


gtt aca gat gag atg gtc aga cta aac tgg ctg acg gaa ttt atg cct   240
Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro
65                  70                  75                  80


ctt ccg acc atc aag cat ttt atc cgt act cct gat gat gca tgg tta   288
Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu
                85                  90                  95


ctc acc act gcg atc ccc ggg aaa aca gca ttc cag gta tta gaa gaa   336
Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu
            100                 105                 110
```

```
tat cct gat tca ggt gaa aat att gtt gat gcg ctg gca gtg ttc ctg          384
Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu
        115                 120                 125

cgc cgg ttg cat tcg att cct gtt tgt aat tgt cct ttt aac agc gat          432
Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp
        130                 135                 140

cgc gta ttt cgt ctc gct cag gcg caa tca cga atg aat aac ggt ttg          480
Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu
145                 150                 155                 160

gtt gat gcg agt gat ttt gat gac gag cgt aat ggc tgg cct gtt gaa          528
Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu
                165                 170                 175

caa gtc tgg aaa gaa atg cat aag ctt ttg cca ttc tca ccg gat tca          576
Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser
                180                 185                 190

gtc gtc act cat ggt gat ttc tca ctt gat aac ctt att ttt gac gag          624
Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu
        195                 200                 205

ggg aaa tta ata ggt tgt att gat gtt gga cga gtc gga atc gca gac          672
Gly Lys Leu Ile Gly Cys Ile Asp Val Gly Arg Val Gly Ile Ala Asp
        210                 215                 220

cga tac cag gat ctt gcc atc cta tgg aac tgc ctc ggt gag ttt tct          720
Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser
225                 230                 235                 240

cct tca tta cag aaa cgg ctt ttt caa aaa tat ggt att gat aat cct          768
Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro
                245                 250                 255

gat atg aat aaa ttg cag ttt cat ttg atg ctc gat gag ttt ttc            813
Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe
                260                 265                 270
```

<210> 7
<211> 271
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
     synthetic construct

<400> 7
Met Ser His Ile Gln Arg Glu Thr Ser Cys Ser Arg Pro Arg Leu Asn
1   5   10   15
Ser Asn Met Asp Ala Asp Leu Tyr Gly Tyr Lys Trp Ala Arg Asp Asn
                20   25   30

Val Gly Gln Ser Gly Ala Thr Ile Tyr Arg Leu Tyr Gly Lys Pro Asp
          35   40   45
Ala Pro Glu Leu Phe Leu Lys His Gly Lys Gly Ser Val Ala Asn Asp
      50   55   60
Val Thr Asp Glu Met Val Arg Leu Asn Trp Leu Thr Glu Phe Met Pro
65   70   75   80
Leu Pro Thr Ile Lys His Phe Ile Arg Thr Pro Asp Asp Ala Trp Leu
                  85   90   95
Leu Thr Thr Ala Ile Pro Gly Lys Thr Ala Phe Gln Val Leu Glu Glu
              100   105   110
Tyr Pro Asp Ser Gly Glu Asn Ile Val Asp Ala Leu Ala Val Phe Leu
          115   120   125
Arg Arg Leu His Ser Ile Pro Val Cys Asn Cys Pro Phe Asn Ser Asp
      130   135   140
Arg Val Phe Arg Leu Ala Gln Ala Gln Ser Arg Met Asn Asn Gly Leu
145   150   155   160
Val Asp Ala Ser Asp Phe Asp Asp Glu Arg Asn Gly Trp Pro Val Glu
              165   170   175
Gln Val Trp Lys Glu Met His Lys Leu Leu Pro Phe Ser Pro Asp Ser
          180   185   190
Val Val Thr His Gly Asp Phe Ser Leu Asp Asn Leu Ile Phe Asp Glu
          195   200   205
Gly Lys Leu Ile Gly Cys Ile Asp Val Gly Arg Val Gly Ile Ala Asp
      210   215   220
Arg Tyr Gln Asp Leu Ala Ile Leu Trp Asn Cys Leu Gly Glu Phe Ser
225   230   235   240
Pro Ser Leu Gln Lys Arg Leu Phe Gln Lys Tyr Gly Ile Asp Asn Pro
              245   250   255
Asp Met Asn Lys Leu Gln Phe His Leu Met Leu Asp Glu Phe Phe
          260   265   270

<210> 8
<211> 5076
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 8
ataggcggcg catgagagaa gcccagacca attacctacc caaaatggag aaagttcacg   60
ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg   120
aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc   180
tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa   240
gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat   300
gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg   360
aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc   420
ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc   480
aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc ctataactct ctacggctaa   540
cctgaatgga ctacgacata gtctagtccg ccaagatgtt cccgttccag ccaatgtatc   600
cgatgcagcc aatgccctat cgcaacccgt tcgcggcccc gcgcaggccc tggttcccca   660
gaaccgaccc ttttctggcg atgcaggtgc aggaattaac ccgctcgatg gctaacctga   720
cgttcaagca acgccgggac gcgccacctg aggggccatc cgctaagaaa ccgaagaagg   780
aggcctcgca aaaacagaaa gggggaggcc aagggaagaa gaagaagaac caagggagaa   840
gaaggctaa gacagggccg cctaatccga aggcacagaa tggaaacaag aagaagacca   900
acaagaaacc aggcaagaga cagcgcatgg tcatgaaatt ggaatctgac aagacgttcc   960

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caatcatgtt ggaagggaag ataaacggct acgcttgtgt ggtcggaggg aagttattca   1020
ggccgatgca tgtggaaggc aagatcgaca acgacgttct ggccgcgctt aagacgaaga   1080
aagcatccaa atacgatctt gagtatgcag atgtgccaca gaacatgcgg gccgatacat   1140
tcaaatacac ccatgagaaa ccccaaggct attacagctg gcatcatgga gcagtccaat   1200
atgaaaatgg gcgtttcacg gtgccgaaag gagttggggc caagggagac agcggacgac   1260
ccattctgga taaccaggga cgggtggtcg ctattgtgct gggaggtgtg aatgaaggat   1320
ctaggacagc cctttcagtc gtcatgtgga acgagaaggg agttaccgtg aagtatactc   1380
cggagaactg cgagcaatgg tcactagtga ccaccatgtg tctgctcgcc aatgtgacgt   1440
tcccatgtgc tcaaccacca atttgctacg acagaaaacc agcagagact ttggccatgc   1500
tcagcgttaa catccctgct gggaggatca gccgtaatta ttataattgg cttggtgctg   1560
gctactattg tggccatgta cgtgctgacc aaccagaaac ataattgaat acagcagcaa   1620
ttggcaagct gcttacatag aactcgcggc gattggcatg ccgctttaaa atttttattt   1680
tattttcttt ttcttttccg aatcggattt tgttttttaat atttcaaaaa aaaaaaaaaa   1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggaagagcg cggccgcgcg ctgggctacg   1800
tcttgctggc gttcgcgacg cgaggctgga tggccttccc cattatgatt cttctcgctt   1860
ccggcggcat cgggatgccc gcgttgcagg ccatgctgtc caggcaggta gatgacgacc   1920
atcagggaca gcttcaagga tcgctcgcgg ctcttaccag cctaacttcg atcactggac   1980
cgctgatcgt cacggcgatt tatgccgcct cggcgagcac atggaacggg ttggcatgga   2040
ttgtaggcgc cgccctatac cttgtctgcc tccccgcgtt gcgtcgcggt gcatggagcc   2100
gggccacctc gacctgaatg gaagccggcg gcacctcgct aacggattca ccactccaag   2160
aattggagcc aatcaattct tgcggagaac tgtgaatgcg caaaccaacc cttggcagaa   2220
catatccatc gcgtccgcca tctccagcag ccgcacgcgg cgcatctcgg cagcgttgg   2280
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accctgagtg attttttctct ggtcccgccg catccatacc gccagttgtt taccctcaca   2640
acgttccagt aaccgggcat gttcatcatc agtaacccgt atcgtgagca tcctctctcg   2700
tttcatcggt atcattaccc ccatgaacag aaatcccccct tacacggagg catcagtgac   2760
caaacaggaa aaaaccgccc ttaacatggc ccgctttatc agaagccaga cattaacgct   2820
tctggagaaa ctcaacgagc tggacgcgga tgaacaggca gacatctgtg aatcgcttca   2880
cgaccacgct gatgagcttt accgcagctg cctcgcgcgt ttcggtgatg acggtgaaaa   2940
cctctgacac atgcagctcc cggagacggt cacagcttgt ctgtaagcgg atgccgggag   3000
cagacaagcc cgtcagggcg cgtcagcggg tgttggcggg tgtcggggcg cagccatgac   3060
ccagtcacgt agcgatagcg gagtgtatac tggcttaact atgcggcatc agagcagatt   3120
gtactgagag tgcaccatat atgcggtgtg aaataccgca cagatgcgta aggagaaaat   3180
accgcatcag gcgctcttcc gcttcctcgc tcactgactc gctgcgctcg tcgttcggc   3240
tgcggcgagc ggtatcagct cactcaaagg cggtaatacg gttatccaca gaatcagggg   3300
ataacgcagg aaagaacatg tgagcaaaag gccagcaaaa ggccaggaac cgtaaaaagg   3360
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gaagctccct cgtgcgctct cctgttccga ccctgccgct taccggatac ctgtccgcct   3540
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gcgccttatc cggtaactat cgtcttgagt ccaacccggt aagacacgac ttatcgccac   3720
tggcagcagc cactggtaac aggattagca gagcgaggta tgtaggcggt gctacagagt   3780
tcttgaagtg gtggcctaac tacggctaca ctagaaggac agtatttggt atctgcgctc   3840
tgctgaagcc agttaccttc ggaaaaagag ttggtagctc ttgatccggc aaacaaacca   3900
ccgctggtag cggtggtttt tttgtttgca agcagcagat tacgcgcaga aaaaaggat   3960
ctcaagaaga tcctttgatc ttttctacgg ggtctgacgc tcagtggaac gaaaactcac   4020
gttaagggat tttggtcatg aacaataaaa ctgtctgctt acataaacag taatacaagg   4080
ggtgttatga gccatattca acgggaaacg tcttgctcga ggccgcgatt aaattccaac   4140
atggatgctg attttatatgg gtataaatgg gctcgcgata atgtcgggca atcaggtgcg   4200
acaatctatc gattgtatgg gaagcccgat cgccagagt tgtttctgaa acatggcaaa   4260
ggtagcgttg ccaatgatgt tacagatgag atggtcagac taaactggct gacggaattt   4320
atgcctcttc cgaccatcaa gcattttatc cgtactcctg atgatgcatg gttactcacc   4380
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actgcgatcc ccgggaaaac agcattccag gtattagaag aatatcctga ttcaggtgaa    4440
aatattgttg atgcgctggc agtgttcctg cgccggttgc attcgattcc tgtttgtaat    4500
tgtcctttta acagcgatcg cgtatttcgt ctcgctcagg cgcaatcacg aatgaataac    4560
ggtttggttg atgcgagtga ttttgatgac gagcgtaatg gctggcctgt tgaacaagtc    4620
tggaaagaaa tgcataagct tttgccattc tcaccggatt cagtcgtcac tcatggtgat    4680
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cgagtcggaa tcgcagaccg ataccaggat cttgccatcc tatggaactg cctcggtgag    4800
ttttctcctt cattacagaa acggcttttt caaaaatatg gtattgataa tcctgatatg    4860
aataaattgc agtttcattt gatgctcgat gagttttct aagaattctc atgtttgaca    4920
gcttatcatc gataagcttt aatgcggtag tttatcacag ttaaattgct aacgcagtca    4980
ggcaccgtgt atgaaatcta acaatgcgct catcgtcatc ctcggcaccg tcaccctgga    5040
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<210> 9
<211> 1026
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<221> CDS
<222> (1)...(1026)

<400> 9

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atg ttc ccg ttc cag cca atg tat ccg atg cag cca atg ccc tat cgc    48
Met Phe Pro Phe Gln Pro Met Tyr Pro Met Gln Pro Met Pro Tyr Arg
 1               5                  10                  15

aac ccg ttc gcg gcc ccg cgc agg ccc tgg ttc ccc aga acc gac cct    96
Asn Pro Phe Ala Ala Pro Arg Arg Pro Trp Phe Pro Arg Thr Asp Pro
            20                  25                  30

ttt ctg gcg atg cag gtg cag gaa tta acc cgc tcg atg gct aac ctg    144
Phe Leu Ala Met Gln Val Gln Glu Leu Thr Arg Ser Met Ala Asn Leu
        35                  40                  45

acg ttc aag caa cgc cgg gac gcg cca cct gag ggg cca tcc gct aag    192
Thr Phe Lys Gln Arg Arg Asp Ala Pro Pro Glu Gly Pro Ser Ala Lys
    50                  55                  60

aaa ccg aag aag gag gcc tcg caa aaa cag aaa ggg gga ggc caa ggg    240
Lys Pro Lys Lys Glu Ala Ser Gln Lys Gln Lys Gly Gly Gly Gln Gly
65                  70                  75                  80

aag aag aag aag aac caa ggg aag aag aag gct aag aca ggg ccg cct    288
Lys Lys Lys Lys Asn Gln Gly Lys Lys Lys Ala Lys Thr Gly Pro Pro
                85                  90                  95
```

```
aat ccg aag gca cag aat gga aac aag aag aag acc aac aag aaa cca      336
Asn Pro Lys Ala Gln Asn Gly Asn Lys Lys Lys Thr Asn Lys Lys Pro
        100                 105                 110

ggc aag aga cag cgc atg gtc atg aaa ttg gaa tct gac aag acg ttc      384
Gly Lys Arg Gln Arg Met Val Met Lys Leu Glu Ser Asp Lys Thr Phe
        115                 120                 125

cca atc atg ttg gaa ggg aag ata aac ggc tac gct tgt gtg gtc gga      432
Pro Ile Met Leu Glu Gly Lys Ile Asn Gly Tyr Ala Cys Val Val Gly
        130                 135                 140

ggg aag tta ttc agg ccg atg cat gtg gaa ggc aag atc gac aac gac      480
Gly Lys Leu Phe Arg Pro Met His Val Glu Gly Lys Ile Asp Asn Asp
145                 150                 155                 160

gtt ctg gcc gcg ctt aag acg aag aaa gca tcc aaa tac gat ctt gag      528
Val Leu Ala Ala Leu Lys Thr Lys Lys Ala Ser Lys Tyr Asp Leu Glu
        165                 170                 175

tat gca gat gtg cca cag aac atg cgg gcc gat aca ttc aaa tac acc      576
Tyr Ala Asp Val Pro Gln Asn Met Arg Ala Asp Thr Phe Lys Tyr Thr
        180                 185                 190

cat gag aaa ccc caa ggc tat tac agc tgg cat cat gga gca gtc caa      624
His Glu Lys Pro Gln Gly Tyr Tyr Ser Trp His His Gly Ala Val Gln
        195                 200                 205

tat gaa aat ggg cgt ttc acg gtg ccg aaa gga gtt ggg gcc aag gga      672
Tyr Glu Asn Gly Arg Phe Thr Val Pro Lys Gly Val Gly Ala Lys Gly
        210                 215                 220

gac agc gga cga ccc att ctg gat aac cag gga cgg gtg gtc gct att      720
Asp Ser Gly Arg Pro Ile Leu Asp Asn Gln Gly Arg Val Val Ala Ile
225                 230                 235                 240

gtg ctg gga ggt gtg aat gaa gga tct agg aca gcc ctt tca gtc gtc      768
Val Leu Gly Gly Val Asn Glu Gly Ser Arg Thr Ala Leu Ser Val Val
        245                 250                 255

atg tgg aac gag aag gga gtt acc gtg aag tat act ccg gag aac tgc      816
Met Trp Asn Glu Lys Gly Val Thr Val Lys Tyr Thr Pro Glu Asn Cys
        260                 265                 270

gag caa tgg tca cta gtg acc acc atg tgt ctg ctc gcc aat gtg acg      864
Glu Gln Trp Ser Leu Val Thr Thr Met Cys Leu Leu Ala Asn Val Thr
        275                 280                 285

ttc cca tgt gct caa cca cca att tgc tac gac aga aaa cca gca gag      912
Phe Pro Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu
        290                 295                 300

act ttg gcc atg ctc agc gtt aac atc cct gct ggg agg atc agc cgt      960
Thr Leu Ala Met Leu Ser Val Asn Ile Pro Ala Gly Arg Ile Ser Arg
305                 310                 315                 320
```

```
aat tat tat aat tgg ctt ggt gct ggc tac tat tgt ggc cat gta cgt     1008
Asn Tyr Tyr Asn Trp Leu Gly Ala Gly Tyr Tyr Cys Gly His Val Arg
            325                 330                 335

gct gac caa cca gaa aca                                              1026
Ala Asp Gln Pro Glu Thr
            340
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<210> 10
<211> 342
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 10

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Met Phe Pro Phe Gln Pro Met Tyr Pro Met Gln Pro Met Pro Tyr Arg
 1               5                  10                  15
Asn Pro Phe Ala Ala Pro Arg Arg Pro Trp Phe Pro Arg Thr Asp Pro
            20                  25                  30
Phe Leu Ala Met Gln Val Gln Glu Leu Thr Arg Ser Met Ala Asn Leu
            35                  40                  45
Thr Phe Lys Gln Arg Arg Asp Ala Pro Pro Glu Gly Pro Ser Ala Lys
        50                  55                  60
Lys Pro Lys Lys Glu Ala Ser Gln Lys Gln Lys Gly Gly Gly Gln Gly
65                  70                  75                  80
Lys Lys Lys Lys Asn Gln Gly Lys Lys Lys Ala Lys Thr Gly Pro Pro
                85                  90                  95
Asn Pro Lys Ala Gln Asn Gly Asn Lys Lys Lys Thr Asn Lys Lys Pro
            100                 105                 110
Gly Lys Arg Gln Arg Met Val Met Lys Leu Glu Ser Asp Lys Thr Phe
            115                 120                 125
Pro Ile Met Leu Glu Gly Lys Ile Asn Gly Tyr Ala Cys Val Val Gly
            130                 135                 140
Gly Lys Leu Phe Arg Pro Met His Val Glu Gly Lys Ile Asp Asn Asp
145                 150                 155                 160
Val Leu Ala Ala Leu Lys Thr Lys Lys Ala Ser Lys Tyr Asp Leu Glu
            165                 170                 175
Tyr Ala Asp Val Pro Gln Asn Met Arg Ala Asp Thr Phe Lys Tyr Thr
            180                 185                 190
His Glu Lys Pro Gln Gly Tyr Tyr Ser Trp His His Gly Ala Val Gln
            195                 200                 205
Tyr Glu Asn Gly Arg Phe Thr Val Pro Lys Gly Val Gly Ala Lys Gly
            210                 215                 220
Asp Ser Gly Arg Pro Ile Leu Asp Asn Gln Gly Arg Val Val Ala Ile
225                 230                 235                 240
Val Leu Gly Gly Val Asn Glu Gly Ser Arg Thr Ala Leu Ser Val Val
            245                 250                 255
Met Trp Asn Glu Lys Gly Val Thr Val Lys Tyr Thr Pro Glu Asn Cys
            260                 265                 270
Glu Gln Trp Ser Leu Val Thr Thr Met Cys Leu Leu Ala Asn Val Thr
            275                 280                 285
```

```
Phe Pro Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu
    290                 295             300
Thr Leu Ala Met Leu Ser Val Asn Ile Pro Ala Gly Arg Ile Ser Arg
305                 310             315             320
Asn Tyr Tyr Asn Trp Leu Gly Ala Gly Tyr Tyr Cys Gly His Val Arg
                325             330             335
Ala Asp Gln Pro Glu Thr
                340
```

<210> 11
<211> 6989
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 11

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ttgacatcga ggaagacagc ccattcctca gagctttgca gcggagcttc ccgcagtttg    120
aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc    180
tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa    240
gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat    300
gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg    360
aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc    420
ctgacctgga aactgagact atgtgcctcc acgacgacga gtcgtgtcgc tacgaagggc    480
aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc ctataactct ctacggctaa    540
cctgaatgga ctacgacata gtctagtccg ccaagatgtc actagtgacc accatgtgtc    600
tgctcgccaa tgtgacgttc ccatgtgctc aaccaccaat ttgctacgac agaaaaccag    660
cagagacttt ggccatgctc agcgttaacg ttgacaaccc gggctacgat gagctgctgg    720
aagcagctgt taagtgcccc ggaaggaaaa ggagatccac cgaggagctg tttaaggagt    780
ataagctaac gcgcccttac atggccagat gcatcagatg tgcagttggg agctgccata    840
gtccaatagc aatcgaggca gtaaagagcg acgggcacga cggttatgtt agacttcaga    900
cttcctcgca gtatggcctg gattcctccg gcaacttaaa gggcaggacc atgcggtatg    960
acatgcacgg gaccattaaa gagataccac tacatcaagt gtcactccat acatctcgcc   1020
cgtgtcacat tgtggatggg cacggttatt tcctgcttgc caggtgcccg gcaggggact   1080
ccatcaccat ggaatttaag aaagattccg tcacacactc ctgctcggtg ccgtatgaag   1140
tgaaatttaa tcctgtaggc agagaactct atactcatcc cccagaacac ggagtagagc   1200
aagcgtgcca agtctacgca catgatgcac agaacagagg agcttatgtc gagatgcacc   1260
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cacctcctgt tgggactagc gccctggtgg aatgcgagtg tggcggcaca aagatctcca   1380
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atcggctgca gaacgataag tgggtgtata attctgacaa actgcccaaa gcagcgggag   1500
ccaccttaaa aggaaaactg catgtcccat tcttgctggc agacggcaaa tgcaccgtgc   1560
ctctagcacc agaacctatg ataaccttcg gtttcagatc agtgtcactg aaactgcacc   1620
ctaagaatcc cacatatcta accacccgcc aacttgctga tgagcctcac tacacgcatg   1680
agctcatatc tgaaccagct gttaggaatt ttaccgtcac cggaaaaggg tgggagtttg   1740
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tgggtttgtc aatttgtgcc gccattgcaa ccgtttccgt tgcagcgtct acctggctgt   1920
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cattttgtct ggctgtgctt tgctgcgccc gcactgcccg gccgagacc acctgggagt   2040
ccttggatca cctatggaac aataaccaac agatgttctg gattcaattg ctgatccctc   2100
tggccgcctt gatcgtagtg actcgcctgc tcaggtgcgt gtgctgtgtc gtgccttttt   2160
tagtcatggc cggcgccgca ggcgccggcg cctacgagca cgcgaccacg atgccgagcc   2220
aagcgggaat ctcgtataac actatagtca acagagcagg ctacgcacca ctccctatca   2280
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gcataacacc aacaaagatc aagctgatac ctacagtgaa cttggagtac gtcacctgcc    2340
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```
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tgtatgaaat ctaacaatgc gctcatcgtc atcctcggca ccgtcaccct ggatgctgtc    6960
tagaggatcc ctaatacgac tcactatag                                       6989
```

<210> 12
<211> 2943
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<221> CDS
<222> (1)...(2943)

<400> 12
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Met Ser Leu Val Thr Thr Met Cys Leu Leu Ala Asn Val Thr Phe Pro
1               5                   10                  15

tgt gct caa cca cca att tgc tac gac aga aaa cca gca gag act ttg    96
Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu Thr Leu
                20                  25                  30

gcc atg ctc agc gtt aac gtt gac aac ccg ggc tac gat gag ctg ctg   144
Ala Met Leu Ser Val Asn Val Asp Asn Pro Gly Tyr Asp Glu Leu Leu
            35                  40                  45

gaa gca gct gtt aag tgc ccc gga agg aaa agg aga tcc acc gag gag   192
Glu Ala Ala Val Lys Cys Pro Gly Arg Lys Arg Arg Ser Thr Glu Glu
        50                  55                  60

ctg ttt aag gag tat aag cta acg cgc cct tac atg gcc aga tgc atc   240
Leu Phe Lys Glu Tyr Lys Leu Thr Arg Pro Tyr Met Ala Arg Cys Ile
65                  70                  75                  80
```

```
aga tgt gca gtt ggg agc tgc cat agt cca ata gca atc gag gca gta          288
Arg Cys Ala Val Gly Ser Cys His Ser Pro Ile Ala Ile Glu Ala Val
                85                      90                      95

aag agc gac ggg cac gac ggt tat gtt aga ctt cag act tcc tcg cag          336
Lys Ser Asp Gly His Asp Gly Tyr Val Arg Leu Gln Thr Ser Ser Gln
                100                     105                     110

tat ggc ctg gat tcc tcc ggc aac tta aag ggc agg acc atg cgg tat          384
Tyr Gly Leu Asp Ser Ser Gly Asn Leu Lys Gly Arg Thr Met Arg Tyr
            115                     120                     125


gac atg cac ggg acc att aaa gag ata cca cta cat caa gtg tca ctc          432
Asp Met His Gly Thr Ile Lys Glu Ile Pro Leu His Gln Val Ser Leu
    130                     135                     140

cat aca tct cgc ccg tgt cac att gtg gat ggg cac ggt tat ttc ctg          480
His Thr Ser Arg Pro Cys His Ile Val Asp Gly His Gly Tyr Phe Leu
145                     150                     155                     160
ctt gcc agg tgc ccg gca ggg gac tcc atc acc atg gaa ttt aag aaa          528
Leu Ala Arg Cys Pro Ala Gly Asp Ser Ile Thr Met Glu Phe Lys Lys
                165                     170                     175

gat tcc gtc aca cac tcc tgc tcg gtg ccg tat gaa gtg aaa ttt aat          576
Asp Ser Val Thr His Ser Cys Ser Val Pro Tyr Glu Val Lys Phe Asn
                180                     185                     190

cct gta ggc aga gaa ctc tat act cat ccc cca gaa cac gga gta gag          624
Pro Val Gly Arg Glu Leu Tyr Thr His Pro Pro Glu His Gly Val Glu
            195                     200                     205

caa gcg tgc caa gtc tac gca cat gat gca cag aac aga gga gct tat          672
Gln Ala Cys Gln Val Tyr Ala His Asp Ala Gln Asn Arg Gly Ala Tyr
    210                     215                     220

gtc gag atg cac ctc cca ggc tca gaa gtg gac agc agt ttg gtt tcc          720
Val Glu Met His Leu Pro Gly Ser Glu Val Asp Ser Ser Leu Val Ser
225                     230                     235                     240

ttg agc ggc agt tca gtc acc gtg aca cct cct gtt ggg act agc gcc          768
Leu Ser Gly Ser Ser Val Thr Val Thr Pro Pro Val Gly Thr Ser Ala
                245                     250                     255

ctg gtg gaa tgc gag tgt ggc ggc aca aag atc tcc aag acc atc aac          816
Leu Val Glu Cys Glu Cys Gly Gly Thr Lys Ile Ser Lys Thr Ile Asn
                260                     265                     270

aag aca aaa cag ttc agc cag tgc aca aag aag gag cag tgc aga gca          864
Lys Thr Lys Gln Phe Ser Gln Cys Thr Lys Lys Glu Gln Cys Arg Ala
            275                     280                     285

tat cgg ctg cag aac gat aag tgg gtg tat aat tct gac aaa ctg ccc          912
Tyr Arg Leu Gln Asn Asp Lys Trp Val Tyr Asn Ser Asp Lys Leu Pro
    290                     295                     300
```

```
aaa gca gcg gga gcc acc tta aaa gga aaa ctg cat gtc cca ttc ttg       960
Lys Ala Ala Gly Ala Thr Leu Lys Gly Lys Leu His Val Pro Phe Leu
305             310             315                 320


ctg gca gac ggc aaa tgc acc gtg cct cta gca cca gaa cct atg ata      1008
Leu Ala Asp Gly Lys Cys Thr Val Pro Leu Ala Pro Glu Pro Met Ile
                325             330             335


acc ttc ggt ttc aga tca gtg tca ctg aaa ctg cac cct aag aat ccc      1056
Thr Phe Gly Phe Arg Ser Val Ser Leu Lys Leu His Pro Lys Asn Pro
                340             345             350


aca tat cta acc acc cgc caa ctt gct gat gag cct cac tac acg cat      1104
Thr Tyr Leu Thr Thr Arg Gln Leu Ala Asp Glu Pro His Tyr Thr His
                355             360             365


gag ctc ata tct gaa cca gct gtt agg aat ttt acc gtc acc gga aaa      1152
Glu Leu Ile Ser Glu Pro Ala Val Arg Asn Phe Thr Val Thr Gly Lys
        370             375             380


ggg tgg gag ttt gta tgg gga aac cac ccg ccg aaa agg ttt tgg gca      1200
Gly Trp Glu Phe Val Trp Gly Asn His Pro Pro Lys Arg Phe Trp Ala
385             390             395                 400


cag gaa aca gca ccc gga aat cca cat ggg cta ccg cac gag gtg ata      1248
Gln Glu Thr Ala Pro Gly Asn Pro His Gly Leu Pro His Glu Val Ile
                405             410             415


act cat tat tac cac aga tac cct atg tcc acc atc ctg ggt ttg tca      1296
Thr His Tyr Tyr His Arg Tyr Pro Met Ser Thr Ile Leu Gly Leu Ser
                420             425             430


att tgt gcc gcc att gca acc gtt tcc gtt gca gcg tct acc tgg ctg      1344
Ile Cys Ala Ala Ile Ala Thr Val Ser Val Ala Ala Ser Thr Trp Leu
        435             440             445


ttt tgc aga tct aga gtt gcg tgc cta act cct tac cgg cta aca cct      1392
Phe Cys Arg Ser Arg Val Ala Cys Leu Thr Pro Tyr Arg Leu Thr Pro
    450             455             460


aac gct agg ata cca ttt tgt ctg gct gtg ctt tgc tgc gcc cgc act      1440
Asn Ala Arg Ile Pro Phe Cys Leu Ala Val Leu Cys Cys Ala Arg Thr
465             470             475                 480


gcc cgg gcc gag acc acc tgg gag tcc ttg gat cac cta tgg aac aat      1488
Ala Arg Ala Glu Thr Thr Trp Glu Ser Leu Asp His Leu Trp Asn Asn
                485             490             495


aac caa cag atg ttc tgg att caa ttg ctg atc cct ctg gcc gcc ttg      1536
Asn Gln Gln Met Phe Trp Ile Gln Leu Leu Ile Pro Leu Ala Ala Leu
                500             505             510


atc gta gtg act cgc ctg ctc agg tgc gtg tgc tgt gtc gtg cct ttt      1584
Ile Val Val Thr Arg Leu Leu Arg Cys Val Cys Cys Val Val Pro Phe
        515             520             525
```

```
tta gtc atg gcc ggc gcc gca ggc gcc ggc gcc tac gag cac gcg acc    1632
Leu Val Met Ala Gly Ala Ala Gly Ala Gly Ala Tyr Glu His Ala Thr
    530             535                 540

acg atg ccg agc caa gcg gga atc tcg tat aac act ata gtc aac aga    1680
Thr Met Pro Ser Gln Ala Gly Ile Ser Tyr Asn Thr Ile Val Asn Arg
545             550                 555                 560


gca ggc tac gca cca ctc cct atc agc ata aca cca aca aag atc aag    1728
Ala Gly Tyr Ala Pro Leu Pro Ile Ser Ile Thr Pro Thr Lys Ile Lys
                565                 570                 575

ctg ata cct aca gtg aac ttg gag tac gtc acc tgc cac tac aaa aca    1776
Leu Ile Pro Thr Val Asn Leu Glu Tyr Val Thr Cys His Tyr Lys Thr
                580                 585                 590

gga atg gat tca cca gcc atc aaa tgc tgc gga tct cag gaa tgc act    1824
Gly Met Asp Ser Pro Ala Ile Lys Cys Cys Gly Ser Gln Glu Cys Thr
            595                 600                 605

cca act tac agg cct gat gaa cag tgc aaa gtc ttc aca ggg gtt tac    1872
Pro Thr Tyr Arg Pro Asp Glu Gln Cys Lys Val Phe Thr Gly Val Tyr
    610                 615                 620

ccg ttc atg tgg ggt ggt gca tat tgc ttt tgc gac act gag aac acc    1920
Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys Asp Thr Glu Asn Thr
625                 630                 635                 640

caa gtc agc aag gcc tac gta atg aaa tct gac gac tgc ctt gcg gat    1968
Gln Val Ser Lys Ala Tyr Val Met Lys Ser Asp Asp Cys Leu Ala Asp
                645                 650                 655

cat gct gaa gca tat aaa gcg cac aca gcc tca gtg cag gcg ttc ctc    2016
His Ala Glu Ala Tyr Lys Ala His Thr Ala Ser Val Gln Ala Phe Leu
            660                 665                 670

aac atc aca gtg gga gaa cac tct att gtg act acc gtg tat gtg aat    2064
Asn Ile Thr Val Gly Glu His Ser Ile Val Thr Thr Val Tyr Val Asn
            675                 680                 685

gga gaa act cct gtg aat ttc aat ggg gtc aaa tta act gca ggt ccg    2112
Gly Glu Thr Pro Val Asn Phe Asn Gly Val Lys Leu Thr Ala Gly Pro
    690                 695                 700

ctt tcc aca gct tgg aca ccc ttt gat cgc aaa atc gtg cag tat gcc    2160
Leu Ser Thr Ala Trp Thr Pro Phe Asp Arg Lys Ile Val Gln Tyr Ala
705                 710                 715                 720

ggg gag atc tat aat tat gat ttt cct gag tat ggg gca gga caa cca    2208
Gly Glu Ile Tyr Asn Tyr Asp Phe Pro Glu Tyr Gly Ala Gly Gln Pro
                725                 730                 735

gga gca ttt gga gat ata caa tcc aga aca gtc tca agc tca gat ctg    2256
Gly Ala Phe Gly Asp Ile Gln Ser Arg Thr Val Ser Ser Ser Asp Leu
            740                 745                 750
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tat gcc aat acc aac cta gtg ctg cag aga ccc aaa gca gga gcg atc     2304
Tyr Ala Asn Thr Asn Leu Val Leu Gln Arg Pro Lys Ala Gly Ala Ile
        755                 760                 765

cac gtg cca tac act cag gca cct tcg ggt ttt gag caa tgg aag aaa     2352
His Val Pro Tyr Thr Gln Ala Pro Ser Gly Phe Glu Gln Trp Lys Lys
        770                 775                 780

gat aaa gct cca tca ttg aaa ttt acc gcc cct ttc gga tgc gaa ata     2400
Asp Lys Ala Pro Ser Leu Lys Phe Thr Ala Pro Phe Gly Cys Glu Ile
785                 790                 795                 800

tat aca aac ccc att cgc gcc gaa aac tgt act gta ggg tca att cca     2448
Tyr Thr Asn Pro Ile Arg Ala Glu Asn Cys Thr Val Gly Ser Ile Pro
                805                 810                 815

tta gcc ttt gac att ccc gac gcc ttg ttc acc agg gtg tca gaa aca     2496
Leu Ala Phe Asp Ile Pro Asp Ala Leu Phe Thr Arg Val Ser Glu Thr
                820                 825                 830

ccg aca ctt tca gcg gcc gaa tgc act ctt aac gag tgc gtg tat tct     2544
Pro Thr Leu Ser Ala Ala Glu Cys Thr Leu Asn Glu Cys Val Tyr Ser
        835                 840                 845

tcc gac ttt ggt ggg atc gcc acg gtc aag tac tcg gcc agc aag tca     2592
Ser Asp Phe Gly Gly Ile Ala Thr Val Lys Tyr Ser Ala Ser Lys Ser
        850                 855                 860

ggc aag tgc gca gtc cat gtg cca tca ggg act gct acc cta aaa gaa     2640
Gly Lys Cys Ala Val His Val Pro Ser Gly Thr Ala Thr Leu Lys Glu
865                 870                 875                 880

gca gca gtc gag cta acc gag caa ggg tcg gcg act atc cat ttc tcg     2688
Ala Ala Val Glu Leu Thr Glu Gln Gly Ser Ala Thr Ile His Phe Ser
                885                 890                 895

acc gca aat atc cac ccg gag ttc agg ctc caa ata tgc aca tca tat     2736
Thr Ala Asn Ile His Pro Glu Phe Arg Leu Gln Ile Cys Thr Ser Tyr
                900                 905                 910

gtt acg tgc aaa ggt gat tgt cac ccc ccg aaa gac cat att gtg aca     2784
Val Thr Cys Lys Gly Asp Cys His Pro Pro Lys Asp His Ile Val Thr
        915                 920                 925

cac cct cag tat cac gcc caa aca ttt aca gcc gcg gtg tca aaa acc     2832
His Pro Gln Tyr His Ala Gln Thr Phe Thr Ala Ala Val Ser Lys Thr
        930                 935                 940

gcg tgg acg tgg tta aca tcc ctg ctg gga gga tca gcc gta att att     2880
Ala Trp Thr Trp Leu Thr Ser Leu Leu Gly Gly Ser Ala Val Ile Ile
945                 950                 955                 960

ata att ggc ttg gtg ctg gct act att gtg gcc atg tac gtg ctg acc     2928
Ile Ile Gly Leu Val Leu Ala Thr Ile Val Ala Met Tyr Val Leu Thr
                965                 970                 975
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aac cag aaa cat aat   2943
Asn Gln Lys His Asn
            980

<210> 13
<211> 981
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 13
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Cys Ala Gln Pro Pro Ile Cys Tyr Asp Arg Lys Pro Ala Glu Thr Leu
            20   25   30
Ala Met Leu Ser Val Asn Val Asp Asn Pro Gly Tyr Asp Glu Leu Leu
        35   40   45
Glu Ala Ala Val Lys Cys Pro Gly Arg Lys Arg Arg Ser Thr Glu Glu
    50   55   60
Leu Phe Lys Glu Tyr Lys Leu Thr Arg Pro Tyr Met Ala Arg Cys Ile
65   70   75   80
Arg Cys Ala Val Gly Ser Cys His Ser Pro Ile Ala Ile Glu Ala Val
                85   90   95
Lys Ser Asp Gly His Asp Gly Tyr Val Arg Leu Gln Thr Ser Ser Gln
            100   105   110
Tyr Gly Leu Asp Ser Ser Gly Asn Leu Lys Gly Arg Thr Met Arg Tyr
        115   120   125
Asp Met His Gly Thr Ile Lys Glu Ile Pro Leu His Gln Val Ser Leu
    130   135   140
His Thr Ser Arg Pro Cys His Ile Val Asp Gly His Gly Tyr Phe Leu
145   150   155   160
Leu Ala Arg Cys Pro Ala Gly Asp Ser Ile Thr Met Glu Phe Lys Lys
                165   170   175
Asp Ser Val Thr His Ser Cys Ser Val Pro Tyr Glu Val Lys Phe Asn
            180   185   190
Pro Val Gly Arg Glu Leu Tyr Thr His Pro Pro Glu His Gly Val Glu
        195   200   205
Gln Ala Cys Gln Val Tyr Ala His Asp Ala Gln Asn Arg Gly Ala Tyr
    210   215   220
Val Glu Met His Leu Pro Gly Ser Glu Val Asp Ser Ser Leu Val Ser
225   230   235   240
Leu Ser Gly Ser Ser Val Thr Val Thr Pro Pro Val Gly Thr Ser Ala
                245   250   255
Leu Val Glu Cys Glu Cys Gly Gly Thr Lys Ile Ser Lys Thr Ile Asn
            260   265   270
Lys Thr Lys Gln Phe Ser Gln Cys Thr Lys Lys Glu Gln Cys Arg Ala
        275   280   285
Tyr Arg Leu Gln Asn Asp Lys Trp Val Tyr Asn Ser Asp Lys Leu Pro
    290   295   300
Lys Ala Ala Gly Ala Thr Leu Lys Gly Lys Leu His Val Pro Phe Leu
305   310   315   320

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Leu Ala Asp Gly Lys Cys Thr Val Pro Leu Ala Pro Glu Pro Met Ile
              325             330             335
Thr Phe Gly Phe Arg Ser Val Ser Leu Lys Leu His Pro Lys Asn Pro
          340             345             350
Thr Tyr Leu Thr Thr Arg Gln Leu Ala Asp Glu Pro His Tyr Thr His
          355             360             365
Glu Leu Ile Ser Glu Pro Ala Val Arg Asn Phe Thr Val Thr Gly Lys
    370             375             380
Gly Trp Glu Phe Val Trp Gly Asn His Pro Pro Lys Arg Phe Trp Ala
385             390             395             400
Gln Glu Thr Ala Pro Gly Asn Pro His Gly Leu Pro His Glu Val Ile
              405             410             415
Thr His Tyr Tyr His Arg Tyr Pro Met Ser Thr Ile Leu Gly Leu Ser
          420             425             430
Ile Cys Ala Ala Ile Ala Thr Val Ser Val Ala Ala Ser Thr Trp Leu
          435             440             445
Phe Cys Arg Ser Arg Val Ala Cys Leu Thr Pro Tyr Arg Leu Thr Pro
    450             455             460
Asn Ala Arg Ile Pro Phe Cys Leu Ala Val Leu Cys Cys Ala Arg Thr
465             470             475             480

Ala Arg Ala Glu Thr Thr Trp Glu Ser Leu Asp His Leu Trp Asn Asn
              485             490             495
Asn Gln Gln Met Phe Trp Ile Gln Leu Leu Ile Pro Leu Ala Ala Leu
          500             505             510
Ile Val Val Thr Arg Leu Leu Arg Cys Val Cys Cys Val Val Pro Phe
          515             520             525
Leu Val Met Ala Gly Ala Ala Gly Ala Gly Ala Tyr Glu His Ala Thr
    530             535             540
Thr Met Pro Ser Gln Ala Gly Ile Ser Tyr Asn Thr Ile Val Asn Arg
545             550             555             560
Ala Gly Tyr Ala Pro Leu Pro Ile Ser Ile Thr Pro Thr Lys Ile Lys
              565             570             575
Leu Ile Pro Thr Val Asn Leu Glu Tyr Val Thr Cys His Tyr Lys Thr
          580             585             590
Gly Met Asp Ser Pro Ala Ile Lys Cys Cys Gly Ser Gln Glu Cys Thr
          595             600             605
Pro Thr Tyr Arg Pro Asp Glu Gln Cys Lys Val Phe Thr Gly Val Tyr
    610             615             620
Pro Phe Met Trp Gly Gly Ala Tyr Cys Phe Cys Asp Thr Glu Asn Thr
625             630             635             640
Gln Val Ser Lys Ala Tyr Val Met Lys Ser Asp Asp Cys Leu Ala Asp
              645             650             655
His Ala Glu Ala Tyr Lys Ala His Thr Ala Ser Val Gln Ala Phe Leu
          660             665             670
Asn Ile Thr Val Gly Glu His Ser Ile Val Thr Thr Val Tyr Val Asn
          675             680             685
Gly Glu Thr Pro Val Asn Phe Asn Gly Val Lys Leu Thr Ala Gly Pro
    690             695             700
Leu Ser Thr Ala Trp Thr Pro Phe Asp Arg Lys Ile Val Gln Tyr Ala
705             710             715             720
Gly Glu Ile Tyr Asn Tyr Asp Phe Pro Glu Tyr Gly Ala Gly Gln Pro
              725             730             735
Gly Ala Phe Gly Asp Ile Gln Ser Arg Thr Val Ser Ser Ser Asp Leu
          740             745             750
Tyr Ala Asn Thr Asn Leu Val Leu Gln Arg Pro Lys Ala Gly Ala Ile
          755             760             765
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```
His Val Pro Tyr Thr Gln Ala Pro Ser Gly Phe Glu Gln Trp Lys Lys
    770             775             780
Asp Lys Ala Pro Ser Leu Lys Phe Thr Ala Pro Phe Gly Cys Glu Ile
785             790             795                 800
Tyr Thr Asn Pro Ile Arg Ala Glu Asn Cys Thr Val Gly Ser Ile Pro
            805             810                 815
Leu Ala Phe Asp Ile Pro Asp Ala Leu Phe Thr Arg Val Ser Glu Thr
            820             825             830
Pro Thr Leu Ser Ala Ala Glu Cys Thr Leu Asn Glu Cys Val Tyr Ser
            835             840             845
Ser Asp Phe Gly Gly Ile Ala Thr Val Lys Tyr Ser Ala Ser Lys Ser
    850             855             860
Gly Lys Cys Ala Val His Val Pro Ser Gly Thr Ala Thr Leu Lys Glu
865             870             875                 880
Ala Ala Val Glu Leu Thr Glu Gln Gly Ser Ala Thr Ile His Phe Ser
            885             890             895
Thr Ala Asn Ile His Pro Glu Phe Arg Leu Gln Ile Cys Thr Ser Tyr
            900             905             910

Val Thr Cys Lys Gly Asp Cys His Pro Pro Lys Asp His Ile Val Thr
    915             920             925
His Pro Gln Tyr His Ala Gln Thr Phe Thr Ala Ala Val Ser Lys Thr
    930             935             940
Ala Trp Thr Trp Leu Thr Ser Leu Leu Gly Gly Ser Ala Val Ile Ile
945             950             955                 960
Ile Ile Gly Leu Val Leu Ala Thr Ile Val Ala Met Tyr Val Leu Thr
            965             970             975
Asn Gln Lys His Asn
            980
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<210> 14
<211> 12379
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 14
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aggtagaagc caagcaggtc actgataatg accatgctaa tgccagagcg ttttcgcatc   180
tggcttcaaa actgatcgaa acggaggtgg acccatccga cacgatcctt gacattggaa   240
gtgcgcccgc ccgcagaatg tattctaagc acaagtatca ttgtatctgt ccgatgagat   300
gtgcggaaga tccggacaga ttgtataagt atgcaactaa gctgaagaaa aactgtaagg   360
aaataactga taaggaattg gacaagaaaa tgaaggagct cgccgccgtc atgagcgacc   420
ctgacctgga aactgagact atgtgcctcc acgacgacga tcgtgtcgc tacgaagggc    480
aagtcgctgt ttaccaggat gtatacgcgg ttgacggacc gacaagtctc tatcaccaag   540
ccaataaggg agttagagtc gcctactgga taggctttga caccacccct tttatgttta   600
agaacttggc tggagcatat ccatcatact ctaccaactg ggccgacgaa accgtgttaa   660
cggctcgtaa catagggccta tgcagctctg acgttatgga gcggtcacgt agagggatgt   720
ccattcttag aaagaagtat ttgaaaccat ccaacaatgt tctattctct gttggctcga   780
ccatctacca cgagaagagg gacttactga ggagctggca cctgccgtct gtatttcact   840
tacgtggcaa gcaaaattac acatgtcggt gtgagactat agttagttgc gacgggtacg   900
tcgttaaaag aatagctatc agtccaggcc tgtatggaa gccttcaggc tatgctgcta    960
cgatgcaccg cgagggattc ttgtgctgca aagtgacaga cacattcaac ggggagaggg  1020
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tggcaacaga tgtcagtgcg gacgacgcgc aaaaactgct ggttgggctc aaccagcgta    1140
tagtcgtcaa cggtcgcacc cagagaaaca ccaataccat gaaaaattac cttttgcccg    1200
tagtggccca ggcatttgct aggtgggcaa aggaatataa ggaagatcaa gaagatgaaa    1260
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atttccactc attcgtgctg cccaggatag gcagtaacac attggagatc gggctgagaa    1440
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<210> 15
<211> 1323
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<221> CDS
<222> (1)...(1323)

<400> 15

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Met Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly
1               5                   10                  15

atg gat ggc cca aag gtt aaa caa tgg ccg tta aca gaa gtg aaa ata    96
Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Val Lys Ile
            20                  25                  30

aaa gca tta aca gca att tgt gaa gaa atg gaa aag gaa gga aaa att    144
Lys Ala Leu Thr Ala Ile Cys Glu Glu Met Glu Lys Glu Gly Lys Ile
        35                  40                  45

aca aaa att ggg cct gaa aat cca tat aac act cca ata ttc gcc ata    192
Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile
        50                  55                  60

aaa aag gaa gac agc act aag tgg aga aaa tta gta gat ttc agg gaa    240
Lys Lys Glu Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu
65                  70                  75                  80
```

```
ctc aat aaa aga act caa gac ttt tgg gag gtt caa tta gga ata cca        288
Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro
            85              90              95

cac cca gca ggg tta aaa aag aaa aaa tca gtg aca gta ctg gat gtg        336
His Pro Ala Gly Leu Lys Lys Lys Lys Ser Val Thr Val Leu Asp Val
            100             105             110

gga gat gca tat ttt tca gtt cct tta gat gaa ggc ttc agg aaa tat        384
Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr
            115             120             125

act gca ttc acc ata cct agt ata aac aat gaa aca cca ggg att aga        432
Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg
    130             135             140

tat caa tat aat gtg ctt cca caa gga tgg aaa ggg tca cca gca ata        480
Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile
145             150             155             160

ttc cag gct agc atg aca aaa atc cta gag ccc ttt aga gct aaa aat        528
Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Ala Lys Asn
            165             170             175

cca gaa ata gtc atc tat caa cat atg gcg gca ttg tat gta gga tct        576
Pro Glu Ile Val Ile Tyr Gln His Met Ala Ala Leu Tyr Val Gly Ser
            180             185             190

gac tta gaa ata ggg caa cat aga gca aaa ata gaa gag tta aga gaa        624
Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Glu
            195             200             205

cat cta tta aag tgg gga ttt acc aca cca gac aaa aaa cat cag aaa        672
His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys
    210             215             220

gaa ccc cca ttt ctt tgg atg ggg tat gaa ctc cat cct gac aaa tgg        720
Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp
225             230             235             240

aca gta cag cct ata cag ctg cca gaa aaa gat agc tgg act gtc aat        768
Thr Val Gln Pro Ile Gln Leu Pro Glu Lys Asp Ser Trp Thr Val Asn
            245             250             255

gac ata cag aag tta gtg gga aaa tta aac tgg aca agt cag att tac        816
Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Thr Ser Gln Ile Tyr
            260             265             270

cca ggg att aaa gta agg caa ctt tgt aag ctc ctt agg ggg acc aaa        864
Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys
            275             280             285

gca cta aca gac ata gta cca cta act gaa gaa gca gaa tta gaa ttg        912
Ala Leu Thr Asp Ile Val Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu
    290             295             300
```

```
gca gag aac agg gaa att cta aaa gaa cca gtg cat gga gta tat tat    960
Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr
305             310             315             320

gac cca tca aaa gac ttg ata gct gaa ata cag aaa cag ggg gat gac    1008
Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Asp Asp
                325             330             335
caa tgg aca tat caa att tac caa gaa cca ttc aaa aac ctg aag aca    1056
Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr
                340             345             350

gga aag tat gca aaa agg agg act acc cac act aat gat gta aaa cag    1104
Gly Lys Tyr Ala Lys Arg Arg Thr Thr His Thr Asn Asp Val Lys Gln
                355             360             365

tta aca gag gca gtg caa aaa ata tcc ttg gaa agc ata gta aca tgg    1152
Leu Thr Glu Ala Val Gln Lys Ile Ser Leu Glu Ser Ile Val Thr Trp
        370             375             380

gga aag act cct aaa ttt aga cta ccc atc caa aaa gaa aca tgg gaa    1200
Gly Lys Thr Pro Lys Phe Arg Leu Pro Ile Gln Lys Glu Thr Trp Glu
385             390             395             400

ata tgg tgg aca gac tat tgg caa gcc aca tgg att cct gag tgg gag    1248
Ile Trp Trp Thr Asp Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu
                405             410             415

ttt gtt aat acc cct ccc cta gta aaa cta tgg tac cag cta gaa aaa    1296
Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys
                420             425             430

gaa ccc ata gca gga gca gaa act ttc                                1323
Glu Pro Ile Ala Gly Ala Glu Thr Phe
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<210> 16
<211> 441
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 16
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Met Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Val Lys Ile
                20              25              30
Lys Ala Leu Thr Ala Ile Cys Glu Glu Met Glu Lys Glu Gly Lys Ile
            35              40              45
Thr Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Ile Phe Ala Ile
        50              55              60
Lys Lys Glu Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu
65              70              75              80
```

```
Leu Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro
            85                  90                  95
His Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu Asp Val
            100             105             110
Gly Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Gly Phe Arg Lys Tyr
        115             120             125
Thr Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg
    130             135             140

Tyr Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile
145             150             155             160
Phe Gln Ala Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Ala Lys Asn
            165             170             175
Pro Glu Ile Val Ile Tyr Gln His Met Ala Ala Leu Tyr Val Gly Ser
            180             185             190
Asp Leu Glu Ile Gly Gln His Arg Ala Lys Ile Glu Glu Leu Arg Glu
        195             200             205
His Leu Leu Lys Trp Gly Phe Thr Thr Pro Asp Lys Lys His Gln Lys
    210             215             220
Glu Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp
225             230             235             240
Thr Val Gln Pro Ile Gln Leu Pro Glu Lys Asp Ser Trp Thr Val Asn
            245             250             255
Asp Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Thr Ser Gln Ile Tyr
            260             265             270
Pro Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys
        275             280             285
Ala Leu Thr Asp Ile Val Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu
    290             295             300
Ala Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr
305             310             315             320
Asp Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Asp Asp
            325             330             335
Gln Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr
            340             345             350

Gly Lys Tyr Ala Lys Arg Arg Thr Thr His Thr Asn Asp Val Lys Gln
        355             360             365
Leu Thr Glu Ala Val Gln Lys Ile Ser Leu Glu Ser Ile Val Thr Trp
    370             375             380
Gly Lys Thr Pro Lys Phe Arg Leu Pro Ile Gln Lys Glu Thr Trp Glu
385             390             395             400
Ile Trp Trp Thr Asp Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu
            405             410             415
Phe Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys
            420             425             430
Glu Pro Ile Ala Gly Ala Glu Thr Phe
        435             440
```

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<210> 17
<211> 13584
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct
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<400> 17

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ggc acc tta ggc ttt tgg atg ata ata att tgt agg gtg gtg ggg aac       96
Gly Thr Leu Gly Phe Trp Met Ile Ile Ile Cys Arg Val Val Gly Asn
                20                  25                  30

ttg aac ttg tgg gtc aca gtc tat tat ggg gta cct gtg tgg aaa gaa      144
Leu Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu
            35                  40                  45

gca aaa act act cta ttc tgt gca tca gat gct aaa gca tat gat aaa      192
Ala Lys Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Lys
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Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
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Asn Pro Arg Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met
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tgg aaa aat gac atg gtg gat cag atg cat gag gat ata atc agt tta      336
Trp Lys Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
                100                 105                 110

tgg gat caa agc cta aaa cca tgt gta aag ttg acc cca ctc tgt gtc      384
Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
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act tta aat tgt aca aat gca cct gcc tac aat aat agc atg cat gga      432
Thr Leu Asn Cys Thr Asn Ala Pro Ala Tyr Asn Asn Ser Met His Gly
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gaa atg aaa aat tgc tct ttc aat aca acc aca gag ata aga gat agg      480
Glu Met Lys Asn Cys Ser Phe Asn Thr Thr Thr Glu Ile Arg Asp Arg
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aaa cag aaa gcg tat gca ctt ttt tat aaa cct gat gta gtg cca ctt      528
Lys Gln Lys Ala Tyr Ala Leu Phe Tyr Lys Pro Asp Val Val Pro Leu
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tgc aat tcc tca acc ata aca caa gcc tgt cca aag gtc act ttt gac     624
Cys Asn Ser Ser Thr Ile Thr Gln Ala Cys Pro Lys Val Thr Phe Asp
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Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys
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Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser
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aca gta caa tgt aca cat gga att atg cca gtg gta tca act caa tta     768
Thr Val Gln Cys Thr His Gly Ile Met Pro Val Val Ser Thr Gln Leu
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ctg tta aat ggt agc cta gca gaa gaa gag ata ata att aga tct gaa     816
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile Ile Ile Arg Ser Glu
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aat ctg aca aac aat atc aaa aca ata ata gtc cac ctt aat aaa tct     864
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gta gaa att gtg tgt aca aga ccc aac aat aat aca aga aaa agt ata     912
Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile
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agg ata gga cca gga caa aca ttc tat gca aca ggt gaa ata ata gga     960
Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile Gly
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aac ata aga gaa gca cat tgt aac att agt aaa agt aac tgg acc agt     1008
Asn Ile Arg Glu Ala His Cys Asn Ile Ser Lys Ser Asn Trp Thr Ser
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Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Thr Lys Leu
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tat gcc cct ccc att gaa gga aac ata aca tgt aaa tca aat atc aca    1296
Tyr Ala Pro Pro Ile Glu Gly Asn Ile Thr Cys Lys Ser Asn Ile Thr
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gga cta cta ttg aca cgt gat gga gga aag aat aca aca aat gag ata    1344
Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Asn Thr Thr Asn Glu Ile
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Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu
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Tyr Lys Tyr Lys Val Val Glu Ile Glu Pro Leu Gly Val Ala Pro Thr
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Lys Ser Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Leu
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            515             520             525

ata gtg caa cag caa agc aat ttg ctg aga gct ata gag gcg caa cag    1632
Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln
            530             535             540

cat atg ttg caa ctc acg gtc tgg ggc att aag cag ctc cag aca aga    1680
His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg
545             550             555             560

gtc ttg gct ata gag aga tac cta aag gat caa cag ctc cta ggg ctt    1728
Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Leu
            565             570             575

tgg ggc tgc tct gga aaa atc atc tgc acc act gct gtg cct tgg aac    1776
Trp Gly Cys Ser Gly Lys Ile Ile Cys Thr Thr Ala Val Pro Trp Asn
            580             585             590

tcc agt tgg agt aat aaa tct caa gaa gat att tgg gat aac atg acc    1824
Ser Ser Trp Ser Asn Lys Ser Gln Glu Asp Ile Trp Asp Asn Met Thr
            595             600             605

tgg atg cag tgg gat aga gaa att agt aat tac aca ggc aca ata tat    1872
Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Gly Thr Ile Tyr
610             615             620
```

```
agg tta ctt gaa gac tcg caa aac cag cag gag aaa aat gaa aaa gat     1920
Arg Leu Leu Glu Asp Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp
625             630             635             640

tta tta gca ttg gac agt tgg aaa aac ttg tgg aat tgg ttt aac ata     1968
Leu Leu Ala Leu Asp Ser Trp Lys Asn Leu Trp Asn Trp Phe Asn Ile
            645             650             655

aca aat tgg ctg tgg tat ata aaa ata ttc atc atg ata gta gga ggc     2016
Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly
            660             665             670

ttg ata ggt ttg aga ata att ttt ggt gta ctc gct ata gtg aaa aga     2064
Leu Ile Gly Leu Arg Ile Ile Phe Gly Val Leu Ala Ile Val Lys Arg
            675             680             685

gtt agg cag gga tac tca cct ttg tcg ttt cag acc ctt acc cca agc     2112
Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Ser
        690             695             700

ccg agg ggt ccc gac agg ctc gga aga atc gaa gaa gaa ggt gga gag     2160
Pro Arg Gly Pro Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu
705             710             715             720

caa gac aaa gac aga tcc att cga tta gtg agc gga ttc tta gca ctt     2208
Gln Asp Lys Asp Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu
            725             730             735

gcc tgg gac gat ctg cgg agc ctg tgc ctc ttc agc tac cac cac ttg     2256
Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His His Leu
            740             745             750

aga gac ttc ata ttg att gca gcg aga gca gcg gaa ctt ctg gga cgc     2304
Arg Asp Phe Ile Leu Ile Ala Ala Arg Ala Ala Glu Leu Leu Gly Arg
            755             760             765

agc agt ctc agg gga ctg cag aga ggg tgg gaa gcc ctt aag tat ctg     2352
Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu
        770             775             780

gga aat ctt gtg cag tat ggg ggt ctg gag cta aaa aga agt gct att     2400
Gly Asn Leu Val Gln Tyr Gly Gly Leu Glu Leu Lys Arg Ser Ala Ile
785             790             795             800

aaa ctg ttt gat acc ata gca ata gca gta gct gaa gga aca gat agg     2448
Lys Leu Phe Asp Thr Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg
            805             810             815

att ctt gaa gta ata cag aga att tgt aga gct atc cgc cac ata cct     2496
Ile Leu Glu Val Ile Gln Arg Ile Cys Arg Ala Ile Arg His Ile Pro
            820             825             830

ata aga ata aga cag ggc ttt gaa gca gct ttg caa                     2532
Ile Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu Gln
            835             840
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<210> 19

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<211> 844
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; Note =
      synthetic construct

<400> 19
Met Arg Val Met Gly Ile Gln Arg Asn Trp Pro Gln Trp Trp Ile Trp
 1               5                  10                  15
Gly Thr Leu Gly Phe Trp Met Ile Ile Ile Cys Arg Val Val Gly Asn
            20                  25                  30
Leu Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu
        35                  40                  45
Ala Lys Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Lys
    50                  55                  60
Glu Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro
65                  70                  75                  80
Asn Pro Arg Glu Ile Val Leu Glu Asn Val Thr Glu Asn Phe Asn Met
                85                  90                  95
Trp Lys Asn Asp Met Val Asp Gln Met His Glu Asp Ile Ile Ser Leu
            100                 105                 110
Trp Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val
        115                 120                 125
Thr Leu Asn Cys Thr Asn Ala Pro Ala Tyr Asn Asn Ser Met His Gly
    130                 135                 140
Glu Met Lys Asn Cys Ser Phe Asn Thr Thr Thr Glu Ile Arg Asp Arg
145                 150                 155                 160
Lys Gln Lys Ala Tyr Ala Leu Phe Tyr Lys Pro Asp Val Val Pro Leu
            165                 170                 175
Asn Arg Arg Glu Glu Asn Asn Gly Thr Gly Glu Tyr Ile Leu Ile Asn
            180                 185                 190
Cys Asn Ser Ser Thr Ile Thr Gln Ala Cys Pro Lys Val Thr Phe Asp
        195                 200                 205
Pro Ile Pro Ile His Tyr Cys Ala Pro Ala Gly Tyr Ala Ile Leu Lys
    210                 215                 220
Cys Asn Asn Lys Thr Phe Asn Gly Thr Gly Pro Cys Asn Asn Val Ser
225                 230                 235                 240
Thr Val Gln Cys Thr His Gly Ile Met Pro Val Val Ser Thr Gln Leu
            245                 250                 255
Leu Leu Asn Gly Ser Leu Ala Glu Glu Glu Ile Ile Ile Arg Ser Glu
            260                 265                 270
Asn Leu Thr Asn Asn Ile Lys Thr Ile Ile Val His Leu Asn Lys Ser
        275                 280                 285
Val Glu Ile Val Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile
    290                 295                 300

Arg Ile Gly Pro Gly Gln Thr Phe Tyr Ala Thr Gly Glu Ile Ile Gly
305                 310                 315                 320
Asn Ile Arg Glu Ala His Cys Asn Ile Ser Lys Ser Asn Trp Thr Ser
            325                 330                 335
Thr Leu Glu Gln Val Lys Lys Lys Leu Lys Glu His Tyr Asn Lys Thr
        340                 345                 350
Ile Glu Phe Asn Pro Pro Ser Gly Gly Asp Leu Glu Val Thr Thr His
        355                 360                 365
```

```
Ser Phe Asn Cys Arg Gly Glu Phe Phe Tyr Cys Asn Thr Thr Lys Leu
    370             375             380
Phe Ser Asn Asn Ser Asp Ser Asn Asn Glu Thr Ile Thr Leu Pro Cys
385             390             395             400
Lys Ile Lys Gln Ile Ile Asn Met Trp Gln Lys Val Gly Arg Ala Met
            405             410             415
Tyr Ala Pro Pro Ile Glu Gly Asn Ile Thr Cys Lys Ser Asn Ile Thr
        420             425             430
Gly Leu Leu Leu Thr Arg Asp Gly Gly Lys Asn Thr Thr Asn Glu Ile
        435             440             445
Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu
    450             455             460
Tyr Lys Tyr Lys Val Val Glu Ile Glu Pro Leu Gly Val Ala Pro Thr
465             470             475             480
Lys Ser Lys Arg Arg Val Val Glu Arg Glu Lys Arg Ala Val Gly Leu
            485             490             495
Gly Ala Val Leu Leu Gly Phe Leu Gly Ala Ala Gly Ser Thr Met Gly
        500             505             510
Ala Ala Ser Ile Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly
        515             520             525
Ile Val Gln Gln Gln Ser Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln
        530             535             540
His Met Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Thr Arg
545             550             555             560
Val Leu Ala Ile Glu Arg Tyr Leu Lys Asp Gln Gln Leu Leu Gly Leu
            565             570             575
Trp Gly Cys Ser Gly Lys Ile Ile Cys Thr Thr Ala Val Pro Trp Asn
        580             585             590
Ser Ser Trp Ser Asn Lys Ser Gln Glu Asp Ile Trp Asp Asn Met Thr
    .   595             600             605
Trp Met Gln Trp Asp Arg Glu Ile Ser Asn Tyr Thr Gly Thr Ile Tyr
    610             615             620
Arg Leu Leu Glu Asp Ser Gln Asn Gln Gln Glu Lys Asn Glu Lys Asp
625             630             635             640
Leu Leu Ala Leu Asp Ser Trp Lys Asn Leu Trp Asn Trp Phe Asn Ile
            645             650             655
Thr Asn Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly
        660             665             670
Leu Ile Gly Leu Arg Ile Ile Phe Gly Val Leu Ala Ile Val Lys Arg
        675             680             685
Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Thr Pro Ser
    690             695             700
Pro Arg Gly Pro Asp Arg Leu Gly Arg Ile Glu Glu Glu Gly Gly Glu
705             710             715             720
Gln Asp Lys Asp Arg Ser Ile Arg Leu Val Ser Gly Phe Leu Ala Leu
            725             730             735

Ala Trp Asp Asp Leu Arg Ser Leu Cys Leu Phe Ser Tyr His His Leu
            740             745             750
Arg Asp Phe Ile Leu Ile Ala Ala Arg Ala Ala Glu Leu Leu Gly Arg
        755             760             765
Ser Ser Leu Arg Gly Leu Gln Arg Gly Trp Glu Ala Leu Lys Tyr Leu
    770             775             780
Gly Asn Leu Val Gln Tyr Gly Gly Leu Glu Leu Lys Arg Ser Ala Ile
785             790             795             800
Lys Leu Phe Asp Thr Ile Ala Ile Ala Val Ala Glu Gly Thr Asp Arg
            805             810             815
```

```
Ile Leu Glu Val Ile Gln Arg Ile Cys Arg Ala Ile Arg His Ile Pro
            820                 825                 830
Ile Arg Ile Arg Gln Gly Phe Glu Ala Ala Leu Gln
        835                 840
```